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Best Local Similarity	99.6%	Pred. No. 0;		
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Db	1	GGTGATTCAGACTCTTCGTGAATGACTTGCAGAGACGACGAGTCACTACTCTTGAAC	60
Qy	117	TTCTCATCTCTCACCCAGGTGATTTGGGAATAATGATGAATCTCTGAGCATCAAC	176
Db	61	TTCTCATCTCTCACCCAGGTGATTTGGGAATAATGATGAATCTCTGAGCATCAAC	120
Qy	177	TCAACAACATGACCAAGAGCCGAATAATGTACTGAAAGAAATGCGTTGTGCATAGTG-	235
Db	121	TCAACAACATGACCAAGAGCCGAATAATGTACTGAAAGAAATGCGTTGTGCATAGTG	180
Qy	236	GCCATCTTCMAAGGGTAAATGTTCTCTCTAAAGTTGATGTAAGCTGAGGCTTGGATGA	295
Db	181	GCCATCTTCMAAGGGTAAATGTTCTCTCTAAAGTTGATGTAAGCTGAGGCTTGGATGA	240
Qy	296	GAAAGTCAGTAAGCAGATTTATAAGGAAGTCAACGGTTCCAAAACATCCAGTACTCTAC	355
Db	241	GAAAGTCAGTAAGCAGATTTATAAGGAAGTCAACGGTTCCAAAACATCCAGTACTCTAC	300
Qy	356	ATGCTTTTGTCACTACAGGGCATGACCAAAAATCTCGACAGCAAAATTTAGATATACATG	415
Db	301	ATGCTTTTGTCACTACAGGGCATGACCAAAAATCTCGACAGCAAAATTTAGATATACATG	360
Qy	416	GCATGACAGACAACCTATTTGAATTGGTCTCTGGAAAAAGAAAAAGAACTAGCCGGTTT	475
Db	361	GCATGACAGACAACCTATTTGAATTGGTCTCTGGAAAAAGAAAAAGAACTAGCCGGTTT	420
Qy	476	AGCATCGATTTGCTAGCATGAAGTCTGTGAAGTCTCGCTTGGCATGTTGGCTGGGA	535
Db	421	AGCATCGATTTGCTAGCATGAAGTCTGTGAAGTCTCGCTTGGCATGTTGGCTGGGA	480
Qy	536	ATTAGCTTATGGAGAAAGAGAAACCTTTCTTTTCCAAATGTTCCACTATGACAGACTT	595
Db	481	ATTAGCTTATGGAGAAAGAGAAACCTTTCTTTTCCAAATGTTCCACTATGACAGACTT	540
Qy	596	GTTATATAGAGTGGAAAGTATTTGGGTTTGATGAAACAAAGAGGGAAAAAGCTCGCAGTGA	655
Db	541	GTTATATAGAGTGGAAAGTATTTGGGTTTGATGAAACAAAGAGGGAAAAAGCTCGCAGTGA	600
Qy	656	TATAGCTGTAGAGAAAGAGTTGGTGCAGCAGACAGAAAGAAAAATGATGGGAATTTCTCT	715
Db	601	TATAGCTGTAGAGAAAGAGTTGGTGCAGCAGACAGAAAGAAAAATGATGGGAATTTCTCT	660
Qy	716	TTTTAAGAGAGAACTGAGAGAAAGCCATGCCAACATGATGAAATTGCCCATAGCATACAT	775
Db	661	TTTTAAGAGAGAACTGAGAGAAAGCCATGCCAACATGATGAAATTGCCCATAGCATACAT	720
Qy	776	GGGGAGAGATTTTATGTTTTCAGCTGTATGAGGAATACACAGATATGCTTTAGCAGTTAA	835
Db	721	GGGGAGAGATTTTATGTTTTCAGCTGTATGAGGAATACACAGATATGCTTTAGCAGTTAA	780
Qy	836	AAACCCATGCGCATCTTAAACATAGCAGCTTGGCTCATCAAATAAAACGATACGATGAAGC	895
Db	781	AAACCCATGCGCATCTTAAACATAGCAGCTTGGCTCATCAAATAAAACGATACGATGAAGC	840
Qy	896	AATTGGTCACTGCAACATTTGTTTGAAGAGAGAGAAAAACCAAAAGCATGTTTCAG	955

Db	841	AATTGTGTCACTCGCAACATTTGTGTTGAAGAAGAAAGAAAAAACCACCAAGACCTGTTTCAG	900
Qy	956	AAGAGGGAAGCAAAAGGCAGAGCTTAGAGACAGATGACTCAGCAGTATGATTTCCGAAA	1015
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Qy	1076	GCAAGAGAAAAGCCTGTATCCAAAAAGCAAGAAAGAAATTCACAAAGGAATTTCAAAAGGAA	1135
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Qy	1136	AGATGAAGTGCTGCTAGTCAAGAGACCTTTTGTGTTAGTATGTTATGCGACATGGTT	1195
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Qy	1196	TGTTTCCCTTTTCTCCCGTATCTTTGCAGCGCACAGATTAAAGCAGATTATGTATGAA	1255
Db	1141	TGTTTCCCTTTTCTCCCGTATCTTTGCAGCGCACAGATTAAAGCAGATTATGTATGAA	1200
Qy	1256	GAAGGTTTACAATT 1269	
Db	1201	GAAGGTTTACAATT 1214	

RESULT 2	
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ID	AAc46130 standard; DNA, 1317 BP.
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DT	18-OCT-2000 (first entry)
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DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 49012.
XX	
KW	Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; 5S.
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XX	
OS	Arabidopsis thaliana.
PN	EP1033405-A2.
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PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
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Query Match 92.3%; Score 1171.6; DB 3; Length 1317;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 1201; Conservative 0; Mismatches 4; Indels 7; Gaps 2;

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 DB 1 TCGATCCAGTCTTGTGATGACTTGCACGACGACGAGTCACTACTCTTGACCTT 60
 QY 119 CTGATCTTCCACGAGTTGATTTGGAAATTAATGATGATCTCTGAGATCAAACTC 178
 DB 61 CTGATCTTCCACGAGTTGATTTGGAAATTAATGATGATCTCTGAGATCAAACTC 114
 QY 179 AAACACATGACCAAGAGAGCGAATTAATTACTGAAAGAGTCCGTTGTGATAGTGC 237
 DB 115 AAACACATGACCAAGAGAGCGAATTAATTACTGAAAGAGTCCGTTGTGATAGTGC 174
 QY 238 CATCTCAAGAGGATTAATGTTCTCTTAAGTTGATGATGAACTGAGTCTTGATGAGA 297
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 QY 358 GCTTTTCTCACTACAGGGCATGACCAAAAACCTGCAGCAACAATTTGAGATACATGCG 417
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 DB 415 CCATCGGTGTTGCTAGCATGAAGTCTGTGAAGCTGCGCTTGTCAATGTTGGCTGGAT 474
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 DB 775 ACCATGCCATCTTAACATAGCAGTCTGCTCAACCACTTAACGATAGATGAACCAA 834
 QY 898 TTGGTCACTGCAACATTGTGTGACAGAGAAAGAGAAAGCCCAAAAGCACTGTTCAAGAA 957

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 QY 958 GAGGAAAGCAAGAGAGAGTATGACATATGATCTCAGACGCTGATGATTTCCGAAAG 1017
 DB 895 GAGGAAAGCAAGAGAGAGTATGACATATGATCTCAGACGCTGATGATTTCCGAAAG 954
 QY 1018 CACAAAGTATGCTCTGACGACAGAGCCATTAAGAGAGTACGACACTTGACAGAGC 1077
 DB 955 CACAAAGTATGCTCTGACGACAGAGCCATTAAGAGAGTACGACACTTGACAGAGC 1014
 QY 1078 AAGAGAAAGCCTTGTACCAAAAGCAGAGAAAGATTAATTAATTAAGAGAGAG 1137
 DB 1015 AAGAGAAAGCCTTGTACCAAAAGCAGAGAAAGATTAATTAATTAAGAGAGAG 1074
 QY 1138 ATGAAGTGTGCTATGATCAAAAGCCTTTTGTGTTGATAGTGTATGCGCAATGTTTG 1197
 DB 1075 ATGAAGTGTGCTATGATCAAAAGCCTTTTGTGTTGATAGTGTATGCGCAATGTTTG 1134
 QY 1198 TTTCCCTTTCTCCCGATCTTTCAGACGACAGAGTTAAAGCAGATTAATGATGAAGA 1257
 DB 1135 TTTCCCTTTCTCCCGATCTTTCAGACGACAGAGTTAAAGCAGATTAATGATGAAGA 1194
 QY 1258 AGGTTACAAAT 1269
 DB 1195 AGGTTACAAAT 1206

RESULT 3
 ID AAA71993 standard; DNA; 3999 BP.
 XX

AC AAA71993;

XX 19-JAN-2001 (first entry)

XX A. thaliana FKBP-like twisted dwarf DNA.

XX Twisted dwarf gene; FKBP; FK506-binding protein; brassinosteroid;

KW plant growth regulator; ethylene-induced gravitropic reaction; root;

KW ethylene-mediated signal transduction; gravitropic; extension growth;

KW plant architecture; immunosuppressant; transgenic plant; ds.

OS Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 1915..3987

FT /*tag= a

FT /product= "FKBP-like twisted dwarf protein"

FT /*tag= b

FT /number= 1

FT intron 1951..2230

FT /*tag= c

FT /number= 1

FT exon 2231..2410

FT /*tag= d

FT /number= 2

FT intron 2411..2525

FT /*tag= e

FT /number= 2

FT exon 2526..2612

FT /*tag= f

FT /number= 3

FT intron 2613..2852

FT /*tag= g

FT /number= 3

FT exon 2853..3038

FT /*tag= h

FT /number= 4

FT intron 3039..3149

FT /*tag= i

FT /number= 4

FT exon 3150..3272

FT		/tag= j
FT		/number= 5
FT	intron	3273. .3412
FT		/tag= k
FT		/number= 5
FT	exon	3413. .3565
FT		/tag= l
FT		/number= 6
FT	intron	3566. .3654
FT		/tag= m
FT		/number= 6
FT	exon	3655. .3987
FT		/tag= n
FT		/number= 7
XX		
PN	DEJ907598-A1.	
PD	24-AUG-2000.	
XX		
PF	22-FEB-1999;	99DE-01007598.
XX		
PR	22-FEB-1999;	99DE-01007598.
PA	(SCHU/) SCHULZ B.	
XX		
DR	WPI; 2000-566218/53.	
DR	P-PSDB; AAB10674.	
XX		
PT	New DNA encoding plant FK506-binding protein analog useful for producing transgenic plants with altered architecture and for studying immunosuppressants.	
PS	Claim 1; Page 10-13; 14pp; German.	
CC	This invention describes a novel DNA sequence (I) containing the coding region for an FKBP (FK506-binding protein)-like twisted dwarf protein (II) of Arabidopsis thaliana which has plant growth regulating activity.	
CC	(I) or their fragments and derivatives are used for transforming prokaryotic or eukaryotic cells, homologous recombination or expression of a non-translated RNA that, by antisense, co-suppression or ribozyme activity, inhibits one or more endogenous FKBP-like genes in a cell, altering the response of plants to brassinosteroids (or their precursors or derivatives) and their signal transduction and reception, for altering ethylene-induced gravitropic reactions in roots or ethylene-mediated signal transduction of the gravitropic stimulus and for altering the extension growth and growth orientation of plants to change plant architecture. Also (I) can be used to identify related sequences in other plants by hybridization under low stringency conditions or by polymerase chain reaction (PCR), and to generate transgenic plants that are useful for studying the activity and signal-transduction processes of immunosuppressants (e.g. FK506, cyclosporin A, rapamycin and related compounds). This sequence encodes the Arabidopsis thaliana FKBP twisted dwarf protein which is described in the method of the invention	
XX		
SQ	Sequence 3999 BP; 1189 A; 697 C; 845 G; 1268 T; 0 U; 0 Other;	
	Query Match 34.7%; Score 440.6; DB 3; Length 3999;	
	Best Local Similarity 69.6%; Pred. No. 3.6e-118;	
	Matches 822; Conservative 0; Mismatches 19; Indels 340; Gaps 3;	
OY	419 TGAGCAGCAACCTATTGAATGTCCTTGGAAAAAGAAAAGAACAATGACCGGTTTAGC	478
Db	2819 TGTGCACATCAAGAGTGAAATGTTGTCGTGAGACACAGAAAAAAGAACATGACCGGTTTAGC	2878
OY	479 CATGGGTGTTGCTACAGTAAGTGTGGTAACGTGCGCTTGTCAGTATGCTGTGGAAAT	538
Db	2879 CATGGGTGTTGCTACAGTAAGTGTGGTAACGTGCGCTTGTCAGTATGCTGTGGAAAT	2938
OY	539 AGCTTATGGAGAAAGAGAAACTTTCTTTCTTTCCAAATGTCACCATATGAGAGACTTGT	598
Db	2939 AGCTTATGGAGAAAGAGAAACTTTCTTTCTTTCCAAATGTCACCATATGAGAGACTTGT	2998
OY	599 ATATGAGTGAAGTATTATGGGTTTGATGAACAAGG-----	636

Db	2999	ATATGAGTGGAACTTATGGGTTTGATGAAACAAAGAGTAACTATTTCCTATACA	3058
QY	637	-----	636
Db	3059	TCATCTTGTTTCTTACCAAGACGCTCCAATCCAGCTTATCCCACTTCCTGCTT	3118
QY	637	-----AGGAAAGCTCCGAGTATATGACTGTAGA	667
Db	3119	ACCTCTCTGACTTAGATGATGATGATTGAAACAGGGGAAAAGCTCGCAGTATATGACTGTAGA	3178
QY	668	GGAAGAAGATTGGTCAGACAGACAGAAAGAAAATGATGGGAATTTCTTTTAAAGAGGA	727
Db	3179	GGAAAGATTTGGTCAGACAGACAGAAAGAAAATGATGGGAATTTCTTTTAAAGAGGA	3238
QY	728	GAACCTGAGAGAACCATGCAACGATGAAAT-----	760
Db	3239	GAACCTGAGAGAACCATGCAACGATGAAATGATTATGATCATCTCTCTATCTATTC	3298
QY	761	-----	760
Db	3399	TCTCTTCCAACAATTACGGTCAAAGTTTAGGTTTCAGGCATATCTTAGTAGCTGCTC	3358
QY	761	-----GGCCATA	767
Db	3359	GAGGCTCTGTGCTCTTCTTTCGGCTTTTGATTAATGCTATGTTTTGCTGTTCAGGCCATA	3418
QY	768	GCATACATGGGGGCGATTTTATGTTTCACTGTATGGGAAGTACAGATATATGCTTTA	827
Db	3419	GCATACATGGGGGCGATTTTATGTTTCACTGTATGGGAAGTACAGATATATGCTTTA	3478
QY	828	GCAGTTAAAAACCATGCCATCTTAAATAGCAGCTTGCTCATCAAACTTAAAAACGATAC	887
Db	3479	GCAGTTAAAAACCATGCCATCTTAAATAGCAGCTTGCTCATCAAACTTAAAAACGATAC	3538
QY	888	GATAGAGCAATTGGTCACTGCAACAT-----	914
Db	3539	GATAGAGCAATTGGTCACTGCAACATTTGTAAGCTATCAAAACCATTCATTGAAGAAA	3598
QY	915	-----GTGT	918
Db	3599	TCATTAAAGTTCACTCGGTTTCTGAAATCTAATCAAACTCAAACTTATCAGGTGT	3658
QY	919	TGACAGAAAGAGAAAAACCCAAAGCACTGTTCAGAAAGGAGAAACAAAGCAGAGC	978
Db	3659	TGACAGAAAGAGAAAAACCCAAAGCACTGTTCAGAAAGGAGAAACAAAGCAGAGC	3718
QY	979	TAGACACGATGGACTCGACACGTGATGATTTCCGAAAGGCAAAAAGTATAGCTCTGACG	1038
Db	3719	TAGACACGATGGACTCGACACGTGATGATTTCCGAAAGGCAAAAAGTATAGCTCTGACG	3778
QY	1039	ACAAGCGATTTAGAAAGAGCTACGACACTTGCAGAGCAAGAGAAAACCTTGTACCAA	1098
Db	3779	ACAAGCGATTTAGAAAGAGCTACGACACTTGCAGAGCAAGAGAAAACCTTGTACCAA	3838
QY	1099	AGCAGAAAGAAATGTACAAAGAAATATTTCAAAGGAAAGTGAAGTGCTGTAGTCAA	1158
Db	3839	AGCAGAAAGAAATGTACAAAGAAATATTTCAAAGGAAAGTGAAGTGCTGTAGTCAA	3898
QY	1159	AGACCTTTTTTGGTGTATGCTGTATAGGCAATGGTTTGTTCCTCTTCCCGTATCT	1218
Db	3899	AGACCTTTTTTGGTGTATGCTGTATAGGCAATGGTTTGTTCCTCTTCCCGTATCT	3958
QY	1219	TTTGACGCCACAGAGTTAAAGCAGATTAATGTATGAAGAAG	1259
Db	3959	TTTGACGCCACAGAGTTAAAGCAGATTAATGTATGAAGAAG	3999
RESULT 4			
ABX88982			
1D	ABX88982 standard; cDNA; 281 BP.		
AC	ABX88982;		

comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 999 sequences (ABN98233-ABN99231), given in the specification or its fragment. A polypeptide (II) encoded by (I), a transgenic plant (III) comprising an exogenous nucleic acid or a genetically modified cell (IV) comprising an exogenous nucleic acid, is useful for screening a candidate agent for its biological effect. (I) is useful in identifying homologous or related genes, in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein and in studying associated physiological pathways. (I) is also useful for the genetic manipulation of cells, particularly plant cells. (I) is also useful in screening assays of various plant strains to determine the strains that are best capable of withstanding a particular disease or environmental stress. (II) and (III) are useful for screening of biologically active agents, e.g. fungicides, insecticides, etc., for elucidating biochemical pathways. The screened agents are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening programs to identify agents that mimic or enhance the action of tolerance factors. Such agents are useful in improved methods of treating crops to enhance their tolerance to environmental stresses. (I) is also useful for enhancing or inhibiting production of a biosynthetic product in a plant. (III) is useful for identifying other mediators that may induce expression of proteins of interest, for establishing the extent to which any specific insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that enhance or induce tolerance to environmental stresses, for identifying factors involved in biosynthetic pathways of nutritional, commercial, or medicinal value and for identifying productions of nutritional, commercial or medicinal value. (IV) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene products. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docid=999909770445

Sequence 968 BP; 260 A; 189 C; 214 G; 305 T; 0 U; 0 Other;

Query Match 10.0%; Score 126.6; DB 6; Length 968;
Best Local Similarity 77.7%; Pred. No. 2.4e-26;
Matches 176; Conservative 0; Mismatches 49; Indels 2; Gaps 2;

QY 436 AATTGCTCTTGGAAAAAGAAAAAGAACTAGCCGGTTTAAAGCCATGGTGTCTTGA 495
DB 68 AATGCTCTTATGAAAGAGATACAGTAATGCGCGTTAGTATGATGTTCCAGCA 127
QY 496 TGAAGTCTGTGAACGTCCTTGTGATGTGCTGGAA-TTACGTTATGGAAAGAA 554
DB 128 TCAAGTCTGTGAACGTCCTTGTGATGTGCTGGAA-TTATGATATAGAGAGAT 187
QY 555 GGAACCTTTTC-TTTTCCCATGTTCCACCTATGGAGACTGTGTATATGAGGGAAGT 613
DB 188 GGAACCTCTTCTTTTCCCATGTTCCATATATGCGGAATGTTAATATGACGTGAAGT 247
QY 614 TATTGGTTTATGAAACAAAGAGGAAAAAGCTCGAGTATGACT 662
DB 248 TGTGGATTGATGAAACAAAGAGGAAAGCTTTTCTTTAAGATCAAT 296

RESULT 6
AAS25522
ID AAS25522 standard; cDNA; 623 BP.

AC AAS25522;

XX 07-NOV-2001 (first entry)

DE Human ovarian PCR-subtracted cDNA library clone #1607.

KM Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
KM gene therapy; cytosolic; T-cell expansion; nucleic acid hybridisation;
KM primer; probe.

XX Homo sapiens.

XX MO200157207-A2.
PN 09-AUG-2001.
PD 05-FEB-2001; 2001WO-US003733.
PF 04-FEB-2000; 2000US-0180403P.
PR 28-MAR-2000; 2000US-0192745P.
XX (CORI-) CORIYA CORP.
PA Algate PA, Mannion J;
PI WPI; 2001-488879/53.
XX New polynucleotides encoding ovarian tumor proteins, useful for treating
PT ovarian cancer, and as probes, primers, and markers of cancer
PT progression.
XX Example 1; Page 373-374; 378pp; English.

XX The invention comprises compositions used for the therapy and diagnosis
CC of ovarian cancer. The compositions comprise one or more ovarian tumor
CC proteins, their associated polynucleotides, or immunogenic portions of
CC the proteins. The ovarian tumor polynucleotides and polypeptides are
CC useful for stimulating and/or expanding T cells specific for a tumor
CC protein. They are also useful for inhibiting the development of cancer in
CC a patient with an ovarian tumor DNA or protein by incubating isolated T-
CC cells allowing them to proliferate, and administering to the patient. The
CC sequences can be used as markers for cancer, for example, to monitor
CC ovarian cancer progression. Probes and primers are useful in nucleic acid
CC hybridisation, in detecting the presence of complementary sequences in a
CC given sample, for preparing mutant species and for preparing other
CC genetic constructions. Sequences AAS252820-AAS25321 and AAS25328-AAS25549
CC represent human ovarian tumor protein cDNA clones

Sequence 623 BP; 226 A; 84 C; 138 G; 175 T; 0 U; 0 Other;

Query Match 4.5%; Score 57.2; DB 4; Length 623;
Best Local Similarity 46.2%; Pred. No. 4.5e-06;
Matches 228; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

QY 662 TGTAGAGAAAGATGTTGTGACAGACAGAAAGAAATGATGGAAATCTCTTTTAA 721
DB 7 TGTAGATTAATTTTATTTAATACAGAAAGACTTAAATGAAATCTTTTCA 66
QY 722 GAGAGAGAACTGGAGAAAGCCATGCAACATGTGAATGGCCATATGATGGGGGA 781
DB 67 ATCCAGAACTGGAGATGGCTATTAATAAATATGCAAGATTTTAAATAC--GTGGA 123
QY 782 CAAATTTATGTTTCACTGATATGGGAAGTACCAAGATATGCTTATGACGATTAACCC 841
DB 124 CAGTTAAAGAGCTGTTATTTAGACAGACATAGAGCAAGCTGCAACTATAGCTTTAAG 183
QY 842 ATGCACTTTAATACATGACAGCTTGTCTCATCAACTAAATCAATAGATGAAGCAATTTG 901
DB 184 CTGTGATCAATATTTGTGCTTTGTAACTGAAGATGTCAATTTGGCAGGAGCAATTTGA 243
QY 902 TCACTGCAACATTTGTGTTGACAGAGAAAGAAACCCAAAGCACTGTTCAAGAGAG 961
DB 244 CAGTTGTTTAGAGGCTCTTGAATATAGACCATCAATATACAAAGCAATGTATGACGAGAG 303
QY 962 GAAAGCAAAAGGACGACTAGACAGATGATGATGATGATGATGATGATGATGATGATGAT 1021
DB 304 TCAAGATGACCAAGATTAAGAAATATGATCAAGATGATGATGATGATGATGATGATGAT 363
QY 1022 AAGTATGCTCCAGAGCAAGGCAATTTGAAGAGAGCTACGAGCACTTGCAGAGCAAGA 1081
DB 364 GGGGATGACGACGAGAGATTAAGCTTTCAGAGGAGATTTGCTGAAGTCAAAAGCAAGAT 423
QY 1082 GAAAGCTTGTATCAAAAGCAGAAAGATGTAACAAAGAAATTTCAAAAGGGAAGATGA 1141


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Db      424  AAGCGACAGAAAAGATTAAGAGAGAGAGATATATGCAAAAATGTTTGGTTAGAAAGATT 483
Oy      1142  AGGTGCTGCTAAGT 1155
          ||| ||| |||
Db      484  CAGTTTGTCTTATT 497

RESULT 7
ADE84891
ID      ADE84891 standard; DNA; 1812 BP.
AC      ADE84891;
XX      29-JAN-2004 (first entry)
DE      Farnesyl transferase inhibitor modulated leukemia associated gene #110.
KW      ss; cyclostatic; farnesyl transferase inhibitor; gene expression;
KW      quinolone; leukemia; cancer.
XX      Homo sapiens.
OS      Homo sapiens.
PN      WO2003038129-A2.
XX      08-MAY-2003.
PD      30-OCT-2002; 2002WO-US034784.
XX      30-OCT-2001; 2001US-033897P.
PR      30-OCT-2001; 2001US-0340081P.
PR      30-OCT-2001; 2001US-0340938P.
PR      30-OCT-2001; 2001US-0341012P.
PA      (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX      Rapont M;
XX      WPI; 2003-513497/48.
XX      Determining whether a patient will respond to treatment with a farnesyl
XX      transferase inhibitor, by analyzing the expression of gene that is
XX      differentially modulated in the presence of the inhibitor.
XX      Disclosure; SEQ ID NO 110; 346pp; English.
XX      The invention relates to a method of determining whether a patient will
XX      respond to treatment with a farnesyl transferase inhibitor (FTI), by
XX      analyzing the expression of gene that is differentially modulated in the
XX      presence of an FTI. The method is useful for determining whether a
XX      patient will respond to treatment with a FTI such as (B)-6-(lamino(4-
XX      chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl)-4-(3-chlorophenyl)-1-
XX      methyl-2-(1H)quinolone, monitoring the therapy of a patient, treating a
XX      patient with leukemia with FTI if the analysis indicates that the patient
XX      will respond. This sequence corresponds to a gene whose expression may be
XX      modulated in the presence of FTI.
XX      Sequence 1812 BP; 550 A; 335 C; 433 G; 493 T; 0 U; 1 Other;

Query Match      4.5%; Score 57.2; DB 9; Length 1812;
Best Local Similarity 46.2%; Pred. No. 7,6e-06;
Matches 228; Conservative 0; Mismatches 263; Indels 3; Gaps

Oy      662  TGTAGAGAAAGGATTGGTGACAGACAGAGAAAGAAATGATGGGAATTCCTTTTAA 721
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      744  TGTAGATATAATTTTATTAATATACAGAGACTTAAAAACATTGGAAATACCTTTTCAA 803

Oy      722  GAGAGAGAAACTGAGAGAAAGCCATGCAACAGTATGAAAATGCCCATAGCATACATGAGGGA 781
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      804  ATCCAGAACTGGGAGATGGCTATTAATAAAAAATATACAGAAAGTTTAAAGTAC--GTGGA 860
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      782  CGATTTTATGTTTCAGCTGTATGGGAAAGTACCAAGATATGCTTTAGCAGTTAAAAACC 841
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      861  CAGTTCAAGGCTGTTTATTGACAGCAGATAGAGCCAAAGCTGCAACCTTATAGCTTTAAG 920
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY	842	ATGCGCATCTTAACATACAGCTGGCTTCATCAAACTAAAAGATAGCATGACGAAATTGG	901
Db	921	CTGTGTACTGATATATGTGTGCTTTGTAACCTGAGATCTCAATTGGCAGGAGCAATTGA	980
QY	902	TCACCTGCACAACTGTGTGTGA CAGAAAGAGAAAAACCCAAAGCACTGTTCAAGAGG	961
Db	981	CAGTTGTTTGAAGGCTCTTGAACTAGACCCATCAAAATACCAAGCACTTGATCGCAAGC	1040
QY	962	GAAGCAAAAGGCGAGCTAGACAGATGACCTCAGCACTGTATGATTTCCGAAAGGCA	1021
Db	1041	TCAAGGATGGCAGAGATTTAAAGAAATATGATCAAGCAATTGGCTGATCTTAAAGAACTCA	1100
QY	1022	AAAGTATGCTCTTGACGACAAAGGCGATTTAGAAAGAGACTACAGCACTTGCAAGCAAG	1081
Db	1101	GGGATATGCACACAGAAATATTAAGCTATCCAGGCGAAATTTGCTGAAGTCAAAACAAAGAT	1160
QY	1082	GAAGCCTTGTACCAAAAGCAGAAAGAAATGTACAAAGAAATATTTCAAAGGAAAGATGA	1141
Db	1161	AAAGGCA CAGAAAGATTAAGAGAAAGCAGATATATGCAAAATATGTTCTTAGAAAGATT	1220
QY	1142	AGGTGGTGTCTAAGT 1155	
Db	1221	CAGTTTGTCTTATT 1234	
RESULT 8			
ABX13847			
ID	ABX13847	standard; DNA; 1380 BP.	
XX	AC		
XX	ABX13847;		
DT	25-FEB-2003	(first entry)	
DE	DNA encoding monoclonal antibody preparation method related protein #3.		
XX			
KW	Transformation; antibody; peptidyl prolyl isomerase; PPIase; human;		
KW	chaperone-like activity; monoclonal antibody preparation; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
XX	Key	Location/Qualifiers	
FT	CDS	1..1380	
FT		/*tag= a	
FT		/product= "Monoclonal antibody preparation method related	
FT		protein #3"	
XX			
FN	JP2002262883-A.		
PD	17-SEP-2002.		
XX			
PF	13-MAR-2001; 2001JP-00070928.		
XX			
PR	13-MAR-2001; 2001JP-00070928.		
XX			
PA	(SEKI) SEKISUI CHEM IND CO LTD.		
XX	(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.		
DR	WI; 2003-132125/13.		
DR	P-PSDB; ABG72858.		
PT	A transformant useful for preparing a monoclonal antibody comprises an		
PT	antibody gene and a gene encoding PPIase.		
XX			
PS	Disclosure; Page 14; 16pp; Japanese.		
XX			
CC	The invention describes a transformant containing an antibody gene and a		
CC	gene encoding a Peptidyl prolyl isomerase (PPIase) having chaperone-like		
CC	activity. The methods detailed using the transformant are useful for the		
CC	preparation of a monoclonal antibody. This sequence encodes a protein		
CC	associated with the method of preparing a monoclonal antibody described		
XX	in the invention		

SQ Sequence 1380 BP; 388 A; 318 C; 414 G; 260 T; 0 U; 0 Other;
 Query Match 4.5%; Score 56.8; DB 7; Length 1380;
 Best Local Similarity 47.5%; Pred. No. 8.7e-06;
 Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GGTTCACCATCGGTGTTGCTAGCATGAAGTCTGTGTAAGCGTGTGTCATGTTGGC 530
 DB 607 GGTTCAGAGAGGCGCATTCAGCGCATGAGAGAGAGAACTTCATCGTACCTCAAG 666
 QY 531 TGGGAATTAGCTTATGAGAAAGAAAGAACTTTCTTTCCCAATGTTCCACTATGCA 590
 DB 667 CCCAGCATATGCTTTTGGCAGGTGGGAGGAAAAGTT---CCAAATCCCAACCAATGCT 723
 QY 591 GACTGTATATAGAGTGAAGTATTTGGGTTTGATGAAACAAAGAGGGGAAAAGCTGCG 650
 DB 724 GAGCTGAAATATGATTAACCTCAAGAGTTTGAAGGCGCAAGAG-----TCT 774
 QY 651 AGTATATGACTGTAGAGAAAGGATTTGTGTCAGACAGACAGAAAGAAATGATGGAAAT 710
 DB 775 TGGGAGATGATTCAGAAAGAGAGCTGGAACAGACACATAGTGAAGAGCGGGGCACT 834
 QY 711 TCTCTTTTAAAGAGAGAAACTGGAGAGCCATGCAACATGTGAATGGCCATAGCA 770
 DB 835 GTGTACTTCAAGAGAGGTAATACAAAGCAAGCTTTACTACATTAAGAGATGTGTCT 894
 QY 771 TACATGGGGAGCATTTTATGTTTCACTGTATGGAGATACCAAGATATGGCTTTAGCA 830
 DB 895 TGGCTGAATATGATGCTAGTTT-----TCCATAGAGAGACAGAAAGCACAGGCC 948
 QY 831 GTTAAAAACCATGCTCTTACATAGCAGCTTGTCTCATCAACTTAAACGATACGAT 890
 DB 949 CTTCGACTGGGCTCTCACTCACTCACTGCGCATGTGTATGTGAACTACAGGCTTCTCT 1008
 QY 891 GAAGCAATTGCTCACTGCAACATTTGTGTGACAGAAAGAGAAAAACCAAGAGCACTG 950
 DB 1009 GCTGCCATTTGAAAGCTTAACAAAGGCCCTAGAACCTGACAGCAACAGAAAGGGCTC 1068
 QY 951 TTCAAGAGAGGAGAAAGAGGAGAGCTAGGACAGATGAGCAAGCTGAGAGGATTTCT 1010
 DB 1069 TTCCGCGGAGAGAGGCGCCACCTGCGCTGATATGATTTGATCTGGACGCGCTGATTTCT 1128
 QY 1011 CGAAAGGACAAAGATATGCTCTGACAGCAAGGCGATTTAGAGAGAGCT 1060
 DB 1129 CAGAAAGGCTCTGACGCTCTACCCCAACAAAGAGCCGCCAAGACCCAGCT 1178

RESULT 9
 AAF21640
 ID AAF21640 standard; DNA; 1903 BP.
 XX
 AC AAF21640;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Human breast and ovarian cancer associated antigen gene SEQ ID 27.
 XX
 KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW neutrophic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
 KW antifungal; antifungal; antiparasitic; cardiant; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO20005173-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005881.

XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-611515/58.
 DR P-PSDB; AAB58737.
 PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention, treatment
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
 PT neurological diseases.
 XX
 PS Claim 1; Page 501; 1299pp; English.
 XX
 CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; neutrophic;
 CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
 CC antiinflammatory; antitumor; vulnery; anticonvulsant; antiparasitic;
 CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
 CC protein sequences are used in the diagnosis of cancer, particularly
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
 CC and agonists may also be used in the diagnosis, prevention and treatment
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemia; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX
 SQ Sequence 1903 BP; 478 A; 470 C; 528 G; 427 T; 0 U; 0 Other;
 Query Match 4.5%; Score 56.8; DB 3; Length 1903;
 Best Local Similarity 47.5%; Pred. No. 1e-05; Indels 18; Gaps 3;
 Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GGTTCACCATCGGTGTTGCTAGCATGAAGTCTGTGTAAGCGTGTGTCATGTTGGC 530
 DB 446 GGTTCAGAGAGGCGCATTCAGCGCATGAGAGAGAGAACTTCATCGTACCTCAAG 505
 QY 531 TGGGAATTAGCTTATGAGAAAGAAAGAACTTTCTTTCCCAATGTTCCACTATGCA 590
 DB 506 CCCAGCATATGCTTTTGGCAGGTGGGAGGAAAAGTT---CCAAATCCCAACCAATGCT 562
 QY 591 GACTGTATATAGAGTGAAGTATTTGGGTTTGATGAAACAAAGAGGGGAAAAGCTGCG 650
 DB 563 GAGCTGAAATATGATTAACCTCAAGAGTTTGAAGGCGCAAGAG-----TCT 613
 QY 651 AGTATATGACTGTAGAGAAAGATTTGTGTCAGACAGACAGAAAGAAATGATGGGAAT 710
 DB 614 TGGGAGATGATTCAGAAAGAGAGCTGGAACAGAGACATAGTGAAGAGCGGGGCACT 673
 QY 711 TCTCTTTTAAAGAGAGAACTGGAGAGCCATGCAACATGTGAATGGCCATAGCA 770
 DB 674 GTGTACTTCAAGAGAGGTAATACAAAGCAAGCTTTCTACATATTAAGAGATCGTGTCT 733
 QY 771 TACATGGGGAGCATTTTATGTTTCACTGTATGGGAATGACAGATATGGCTTTAGCA 830
 DB 734 TGGCTGAATATGATGCTAGTTT-----TCCATAGAGAGACAGAAAGCACAGGCC 787
 QY 831 GTTAAAAACCATGCTCTTACATAGCAGCTTGTGCTCATCAACTTAAACGATACGAT 890
 DB 788 CTTCGACTGGGCTCTCACTCACTCACTGCGCATGTGTATGTGAATACAGGCTTCTCT 847
 QY 891 GAAGCAATTGCTCACTGCAACATTTGTGTGACAGAAAGAGAAAAACCAAGAGCACTG 950

XX Homo sapiens.
OS
XX WO2003004989-A2.
PN
XX
XX 16-JAN-2003.
PD
XX
XX 21-JUN-2002; 2002WO-US019669.
PF
XX
XX 21-JUN-2001; 2001US-0299887P.
PR
XX 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-030501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Lillie J, Gamavarapu M, Glat K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Best RC, Hortobagyi GN, Puzeta L, Merie F, Sahin A, Mills GB;
XX WPI; 2003-210381/20.
XX P-PSDB; ABR47454.
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
XX Claim 1; SEQ ID NO 139; 128bp; English.
XX
XX The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC5034 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2156 BP; 530 A; 551 C; 606 G; 469 T; 0 U; 0 Other;
SQ
Query Match 4.5%; Score 56.8; DB 7; Length 2156;
Best Local Similarity 47.5%; Pred. No. 1.1e-05;
Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;
QY 471 GGTTCACCATCGGTGTTGCTAGCATGAAGTCTGTGAGAGTGGCTGTGTCATGTTGGC 530
DB 706 GGTCTGAGAGGGCGCATTCAGCGCATGAGAGAAACATTCATCGTGTACTCTAAG 765
QY 531 TGGGAATTAAGCTATGAGGAAAGAGAAACCTTTCTTTCCCAATGTTCCACCTATGCA 590
DB 766 CCCAGCTATGCTTTGGCAAGTGGAGAGAAAGTT---CCAAATCCCAACCAATGCT 822
QY 591 GACTTGTATATGAGGTGAGAGTATTTGGGTTTGATGAAACAAAGAGGAGAAAGCTCGC 650
DB 823 GAGCTGAATATGAAATTAACCTCAAGAGTTTGAAGGCGCAAGAG-----TCT 873
QY 651 AGTATATGACTGTAGAGAGAAAGATTTGTGTCAGACAGACAGAGAGAAATATGATGGAAT 710
DB 874 TGGAGATGATTAAGAGAGAAAGCTGAGACCACTATGTAAGAGAGCGGGGACT 933
QY 711 TCTCTTTTAAAGAGAGAAACCTGAGAGAGCCATGCAACAGTATGTAATGGCCATAGCA 770
DB 934 GTGACTTTCAGAGAGAGTAAATACAGCAAGCTTTACTACAGTATTAAGAGATGTGTCT 993
QY 771 TACATGGGGGAGCATTTTATGTTTCACTGTATGGAAGTACAGAGATATGCTTTAGCA 830

DB 994 TGGCTGAATATGAGTCTAGTTT-----TCCAATGAGAGAGACAGAAAGACAGGCC 1047
QY 831 GTTAAAAACCCATGCATCTTAACATAGAGCTGCTCATGAACTAAACGATACAT 890
DB 1048 CTTCGACTGCGCTCTACCTCAACCTGCGCATGTGTGATCTGAACTACAGGCTTCTCT 1107
QY 891 GAAGCAATTTGTCTCATCTGCAACATTTGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAG 950
DB 1108 GCTGCATTTGAAGAGCTGTAAACAGAGCCCTAGAACTGAGACAGAGACAGAGAGAGAGAG 1167
QY 951 TTTCAG 1010
DB 1168 TTCCGCGCGGAG 1227
QY 1011 CGAAAG 1060
DB 1228 CAGAGAGTCTCTGAGCTTACCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1277
RESULT 12
AAV24010 standard; DNA; 2157 BP.
ID AAV24010 standard; DNA; 2157 BP.
XX
XX AAV24010;
XX
XX 06-AUG-1998 (first entry)
XX
XX Human FK506 binding protein, FKBP52, coding sequence.
DE
XX
XX FK506 binding protein; FKBP52; human; immune response regulator;
KW immunosuppressant; steroid hormone receptor transformation; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 100.1479
FT CDS /*tag= a /product= "FKBP52"
XX
XX US5763590-A.
PN
XX
XX 09-JUN-1998.
PD
XX
XX 09-NOV-1994; 94US-00336618.
PF
XX
XX 11-OCT-1991; 91US-00777752.
PR 16-OCT-1992; 92US-00963325.
PR 29-MAR-1994; 94US-00218989.
XX
XX (VERT-) VERTEX PHARM INC.
XX
XX Peattie DA, Livingston DJ, Harding MW;
PI WPI; 1998-347419/30.
DR P-PSDB; AAM54038.
XX
XX DNA sequence encoding human FK506-binding protein - and recombinant DNA
PT molecule containing it.
XX
XX Claim 1; Fig 3; 28bp; English.
XX
XX This sequence encodes 52 kD human FK506 binding protein, referred to as
CC FKBP52, of the invention. The FKBP52 protein plays a key role in
CC regulating immune responses. FKBP52 may be useful for mediating steroid
CC hormone receptor transformation. The DNA may be used to screen for new
CC immunosuppressants, and in assays for metabolites in samples from
CC individuals taking immunosuppressants. The DNA may also be used in assays
CC for identifying natural intracellular rapamycin-like or FK506 like
CC substances, and in assays for identifying natural intracellular
CC substrates that are potential targets for other immunosuppressants
XX
XX Sequence 2157 BP; 531 A; 551 C; 606 G; 469 T; 0 U; 0 Other;
SQ

10266

Query Match 4.5%; Score 56.8; DB 2; Length 2157;
 Best Local Similarity 47.5%; Pred. No. 1.1e-05;
 Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GGTTCACCATCGGTGTTGCTAGCATGAAGCTCTGTAAAGCTGGGCTTGTCATGTTGGC 530
 DB 706 GGTTCAGAGAGGCGCATTCAGCGATGAGAAAGAAACCTTCATCGTGTACTCAAG 765

QY 531 TGGGAATTAAGCTTATGGAAGAAAGAACTTTCTTTCCCAATGTTCCACTATGCA 590
 DB 766 CCCAGCATGCTTTTGGCAGGTGTTGGAGAGAAAGTT---CCAAATCCCAACCAATGCT 822

QY 591 GACTTGTTATATGAGGTGGAAGTTATGCGTTGATGAAACAAAGAGAGGAAAGCTGCG 650
 DB 823 GAGCTGAATATGAAATTAACCTCAAGAGTTTGAAGAGGCAAGG-----TCT 873

QY 651 AGTATATGACTGATGAGAGAAAGATTTGGTCAGACAGACAGAGAAATATGATGGAAAT 710
 DB 874 TGGGAGATGAATTCAGAGAGAAAGCTGGAACAGACACATAGTGAAGAGCGGGGCACT 933

QY 711 TCTCTTTTAAAGAGAGAAACCTGAGAGAGCATGCAAGTATGAAATGGCCATAGCA 770
 DB 934 GTGTACTTCAAGAGAGGTAATTAACAGAGAGCTTACTACGATATAGAGAGATGTGCT 993

QY 771 TACATGGGAGGACGATTTTATGTTTCACTGTATGGAAGTACAGATATGCTTTAGCA 830
 DB 994 TGGCTGAATATGAGTCTAGTTT-----TCCAATGAGAGAGCAAGAAAGCAGAGCC 1047

QY 831 GTTAAAAACCATGCGCATCTTAACATGACAGCTTGCTCATCAACTTAAACGATACAT 890
 DB 1048 CTTGACATGCGCTCTCACTCACTCACTGCGCATGATCTGAAACTACAGGCGCTTCTCT 1107

QY 891 GAAGCAATTTGATCTGCAACATTTGTGTGACAGAGAGAGAAACCAAGAAAGCAGCTG 950
 DB 1108 GCTGCCATTGAAGAGCTTAAACAGGCGCTTGAATGACAGACAGCAACAGAGAGGCTC 1167

QY 951 TTCAAGAGAGGAGAAAGCAAGGAGCTAGACAGATGACATCAAGACGATGATTTTC 1010
 DB 1168 TTCCGCGGGGAGAGGCGCACCTGGCGGTGATGACTTTGAACCTGCAACGGGCTGATTTTC 1227

QY 1011 CGAAAGGACAAAAGTATGCTCTGACGACAGGCGGATTTGAAGAGAGCT 1060
 DB 1228 CAGAAAGTCTCTGACGCTTACCCCAACAGAAAGCCGCCAAGCCAGCT 1277

RESULT 13
 ABZ35317
 ID ABZ35317 standard; cDNA; 2246 BP.
 AC ABZ35317;
 XX
 DT 05-FEB-2003 (first entry)
 XX
 DE Human gene expression profile polynucleotide SEQ ID NO 428.
 DE
 XX Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
 XX bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
 XX tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
 XX gene expression; gene; ss.
 XX
 OS Homo sapiens.
 OS
 PN W0200274979-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-MAR-2002; 2002MO-US008456.
 XX
 PR 20-MAR-2001; 2001US-0276947P.
 XX
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 XX
 PI Wan J, Wang Y;

XX
 DR WPI; 2002-740862/80.
 XX
 PT New gene expression profile generated from primary, endothelial,
 PT epithelial, and muscle cell types, useful for identifying disease
 PT pathologies involving alterations of gene expression, e.g. cancer.
 XX
 PS Example 3; Page 575-576; 850pp; English.

XX
 CC The invention relates to a gene expression profile comprising one or more
 CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
 CC endothelium, myometrium microvascular endothelium, keratinocyte
 CC epithelium, bronchial epithelium, mammary epithelium, prostate
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
 CC small airway epithelium, renal epithelium, umbilical artery smooth
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
 CC osteoblasts or prostate stromal cell. The gene expression profile is used
 CC for determining the level of RNA expression for a sample, determining the
 CC phenotype of a cell and distinguishing cell types. The gene or a protein
 CC expression profile is useful in identifying disease pathologies involving
 CC alterations of gene expression. The assessment of expression profiles may
 CC provide meaningful information with respect to tumour type and stage.
 CC treatment methods, and prognosis. The gene or protein expression profile
 CC may also be used for creating microarrays. The microarray is useful for
 CC genetic and physical mapping of genomes, DNA sequencing, genetic or
 CC medical diagnosis, genotyping of organisms, confirming cell or tissue
 CC identifications and in identifying promising antibiotics, antiviral or
 CC antifungal agents

XX
 SQ Sequence 2246 BP; 547 A; 580 C; 632 G; 487 T; 0 U; 0 Other;

Query Match 4.5%; Score 56.8; DB 6; Length 2246;
 Best Local Similarity 47.5%; Pred. No. 1.1e-05;
 Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GGTTCACCATCGGTGTTGCTAGCATGAAGCTCTGTAAAGCTGGGCTTGTCATGTTGGC 530
 DB 762 GGTCTGAGAGGCGCATTCAGGCGCATGAGAAAGAGAAACATTCATCGTGTACTCAAG 821

QY 531 TGGGAATTAAGCTTATGGAAGAAAGAACTTTCTTTCCCAATGTTCCACTATGCA 590
 DB 822 CCCAGCTATGCTTTTGGCAGGTGTTGGAGAGAAAGTT---CCAAATCCCAACCAATGCT 878

QY 591 GACTTGTTATGAGGTGGAAGTTATGCGTTTGAAGAAACAAAGAGGAGAAAGCTGCG 650
 DB 879 GAGCTGAATATGAAATTAACCTCAAGAGTTTGAAGAGCCCAAGAG-----TCT 929

QY 651 AGTATATGACTGATGAGAGAAAGATTTGTGACAGACAGAGAAAGAAATGATGGGAAT 710
 DB 930 TGGGAGATGAATTCAGAGAGAGAGCTGGAACAGAGACATATGTAAGAGGCGGCACT 989

QY 711 TCTCTTTTAAAGAGAGAAACTGAGAGAGCCATGCAACAGTATGAAATGGCATAGCA 770
 DB 990 GTGTACTTCAAGAGAGTAAATTAACAGCAAGCTTTACTACAGTATGAAGATCGTGTCT 1049

QY 771 TACATGGGAGAGATTTTATGTTTTCAGCTGTATGGAAGTATACAGAGATATGCTTATGCA 830
 DB 1050 TGGCTGAATATGAGTCTAGTTT-----TCCAATGAGAGAGACAGAAAGACAGGCTC 1103

QY 831 GTTAAAAACCATGCGCATCTTAACATAGCAGCTTGCTCATCAACTTAAAGATAGCAT 890
 DB 1104 CTTGACGCGCTCTCACTCAACCTGGCCAGTGTGCATCTGAACCTACAGGCTTCTCT 1163

QY 891 GAAGCAATTTGTCATCTGCAACTTGTGTTGAAGAGAGAGAGAAACCAAGAGCATG 950
 DB 1164 GCTGCCATTGAAGGCTGTAACAGGCGCTTGAACCTGACAGCAACAGAGAGGCGCTTC 1223

QY 951 TTCAAGAGAGGAGAAAGCAAGAGAGATGAGACAGATGACATGATGATTTTC 1010

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Db      1224 TTCCGCGGGGAGAGGCCCACTGGCGGTGATGACTTTGAACTGGACGGGCTGATTTTC 1283
QY      1011 CGAAGGCACAAAAGTATGCTCTCTGACGACAGGCGATTGGAAGAGCT 1060
Db      1284 CAGAAAGTCTGTGACGTCTTACCCCAACAAAGCCGCCCAAGACCCAGCT 1333

RESULT 14
AAQ48515
ID      AAQ48515 standard; cDNA; 2070 BP.
XX
XX      AAQ48515;
AC
XX      25-MAR-2003 (revised)
DT      28-MAR-1994 (first entry)
XX
DE      Encodes rabbit HBI protein which binds hsp90.
XX
KM      steroid hormone receptor; immunosuppressor; FK506; binding protein; FKBP;
KM      heat shock protein; hsp90; chaperone protein; rotamase activity; ss.
XX
OS      Oryctolagus cuniculus.
XX
XX      Key
FH      4.1380
FT      CDS
FT      /*tag= a
FT      /product= "HBI"
XX
XX      WO9318146-A2.
XX
XX      16-SEP-1993.
XX
XX      04-MAR-1993; 93WO-FR000219.
XX
XX      04-MAR-1992; 92FR-00002612.
XX
XX      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX      Lebeau M, Massol N, Renoir M, Radanyi C, Mornon J, Callebaut I;
XX      Bailieu E, Chambraud B;
XX      WPI; 1993-303460/38.
XX      P-PSDB; AAR41781.
XX
XX      New protein forming complex with heat shock protein - also binding immuno
XX      -suppressors, etc., and corresp. nucleic acid antibodies etc., useful
XX      e.g. for detecting tumours, treating auto-immune disease, etc.
XX
XX      Claim 1; Fig 1; 43pp; French.
XX
XX      The HBI protein is able to complex chaperone protein hsp90, even when the
XX      chaperone protein is part of a hetero-oligomer with other proteins. Hsp90
XX      can bind to steroid hormone receptors, vitamin D, and Tyrosine Kinases of
XX      viral oncogenes; HBI is thus useful for the study, prevention or
XX      treatment of diseases associated with dysfunction of proteins which form
XX      complexes with hsp90, e.g. rickets, cancer, dioxin poisoning or
XX      autoimmune disease. HBI can also be used in immunosuppressor research.
XX      The cDNA sequence coding for HBI was isolated by screening a rabbit liver
XX      cDNA library with a probe based on part of a protein known to be present
XX      in a steroid receptor complex. (Updated on 25-MAR-2003 to correct PN
XX      field.)
XX
XX      Sequence 2070 BP; 480 A; 549 C; 620 G; 421 T; 0 U; 0 Other;
SQ
Query Match      4.0%; Score 51.4; DB 2; Length 2070;
Best Local Similarity 46.8%; Pred. No. 0.00041;
Matches 200; Conservative 0; Mismatches 221; Indels 6; Gaps 1;
QY      634 AGAAGGGAAGAGCTGCGAGTATATGACTGTAGAGGAAGATTGGTGCAGACAGAGAA 693
Db      761 AGAAGGCCAAGAGTCTGTGAGATGAGCTCGAGAGAGAAAGCTGAGACAGAGCCCATCG 820

```

```

QY      694 GAAATATGATGGGATTTCTCTTTTAAAGAGAGAACTGAGAGAGCCATGCAAGCT 753
Db      821 TGAAAGAGGAGGCACTGTACTTCAAGAAAGCAATGAAAGAGGCTGTGTACAGT 880
QY      754 ATGAATGGCCATGATATCATGGGGAGAGATTATATGTTTACGCTGTATGGAAATAC 813
Db      881 ACAGAGAGATTTGTCTTGTGGCTGGAAATACAGATCAAGTTTT-----TCCAGTGAAGAG 934
QY      814 AGGATATGGCTTTAGAGTTTAAACCAATGCACTTTAACAATAGCAGCTTCCTCATCA 873
Db      935 TGCAAAAGGACAGAGCCCTGCGCTGCTCCCACTTCAACCTGCTATGTGTACACTTA 994
QY      874 AACTAAACGATACGATGAGCAATTTGTCACCTGCAACATTTGTTGACAGAAAGAGA 933
Db      995 AGCTACAGGCTTCTGCGCAGCCGTGGAAGCTGTAAAGAGCCCTGGAACCTGGAACAGCA 1054
QY      934 AAAACCCAAAGCATCTGTTTCAAGAGGGAAGGAAAGCAAGGACAGACAGATGAGACT 993
Db      1055 ACAACGAGAAAGGCTCTTCCGCGGGGAGAGGCCCACTGCTGTGAACGACTTTGACC 1114
QY      994 CAGCAGTGATGATTTCCGAAAGGCACAAAGATGCTCTGTCAGCAGAGCGATTAGAA 1053
Db      1115 TGACAGGGGTGACTTTCAGAAAGTCTTGCAAGCTTACCTCAGCAACAAAGCGGCTAAG 1174
QY      1054 GAGAGCT 1060
Db      1175 CCCAGCT 1181

RESULT 15
ADA71938
ID      ADA71938 standard; DNA; 2000 BP.
XX
XX      ADA71938;
AC
XX      20-NOV-2003 (first entry)
DT
XX
XX      Rice gene, SEQ ID 5263.
XX
XX      Plant; bacterial infection; fungal infection; viral infection; rice;
XX      gene; ds.
XX
XX      Oryza sativa.
XX
XX      MO2003000898-A1.
XX
XX      03-JAN-2003.
XX
XX      22-JUN-2001; 2001WO-IB001105.
XX
XX      22-JUN-2001; 2001WO-IB001105.
XX
XX      22-JUN-2001; 2001WO-IB001105.
XX
XX      (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX      Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX      Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX      WPI; 2003-175290/17.
XX
XX      Identifying at least one gene involved in plant resistance or response to
XX      pathogenic infection for conferring resistance or tolerance to a plant to
XX      bacterial, fungal or viral infection by determining or detecting plant
XX      gene expression.
XX
XX      Claim 27; SEQ ID NO 5263; 899pp; English.
XX
XX      The present invention relates to a method (M1) for identifying genes
XX      involved in plant resistance or response to pathogenic infection. M1
XX      comprises identifying a gene whose expression is significantly altered in
XX      the incompatible interaction of plant gene expression relative to
XX      expression of the gene in an uninfected plant, in a mutant plant that
XX      does not express a gene associated with response to pathogenic infection,
XX      or in a corresponding incompatible or compatible interaction. (M1) is

```

CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 4.0%; Score 50.4; DB 7; Length 2000;
Best Local Similarity 9.6%; Pred. No. 0.00078;
Matches 66; Conservative 310; Mismatches 301; Indels 11; Gaps 1;

```
QY 478 CCATGGGTGTTGATGATGAAGTCTGTGAACGCGCTTGATGATGCTGGGAAT 537
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 MMRSMCRMSKACCYMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMR 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 538 TAGCTTATGGAAGAAAGAACTTTCTTTCCCAATGTTCCACTATGACAGATTGT 597
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 SCKRARMKRCRSGRAMKRCGCMCRMSYGMWRMSWRMSKRYKMSRMRYMRKK 467
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 598 TATATGAGTGAAGTATTTGGTTTGAACAAGAGAGAAAGCTGCAGTGATA 657
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 468 CSRTTMMGKTRGMMGTMRGRYKRSKMRKRRMRGRMRMRMRMRMRMRMRMR 527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 658 TGACTGTAGAGAAAGATTTGTCAGCAGACAGAGAAAGAAATGATGGAATTCCTTT 717
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 ARKYSYSAARKACMYRGKGYWAGMMWKRYKMYKMMYKRYKSKSYCKMSY 587
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 718 TTAAGAGAGAAAGCTGAGAGAACCATGCAAGTATGAATGCCATAGCATACATGG 777
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 588 ASCSKSARKAGAKKRSKMSKMSKMSKRSKRSKRSKRSKRSKRSKRSKRSK 647
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 778 GGAAGATTTTATGTTTCACTGATGGAAGTACAGATATGAGTATGAGTATTA 837
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 -----WKSYYTCYWRKMSKSTCTMYTMSKTYAKYSYRMYRAMCMYMR 696
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 838 ACCATGCATCTTAACATAGCAGCTTGCCTCATCAACTAAACGATACGATGAGCAA 897
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 697 WYYRYRSYMTYMAWYTSSTRMANTGMKYSGRYTSWYKCKSMKYRSMWYMSMMWAK 756
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 898 TTGCTCACTGCAACTGTGTGACAGAGAGAGAAAGAAAGCAAAAGCACTGTTCA 957
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 757 TWKMMRRYATRRMMWYRYSKMYTCTMGMGMYMMRYMKRMWYKCTKYWYSAT 816
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 958 GAGGAGAGCAAGAGAGAGATGAGACAGATGAGTACAGATGATGATTTCCAAAG 1017
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 817 YMTGTMAAMMMMAKTKRMGMGTGAKTRBARARATYMKATYCATKRMWTKGAKMA 876
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1018 CACAAAAGTATGCTCTGACGACAAAGCGATTGAAGAGAGCTACGACCTTGCA 1077
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 877 MAKAMRYKYSMMWMAWYYYKTRRTYKTCWMAKRWGSMWYMRMMWKSAMMMWKG 936
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1078 AAGAGAAAGCTTGTACCAAAAGCAAGAAAGAAATGTACAAAGAAATTTCAA 1137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 937 WGWTKYMYWYCTTWKMAAGRAIKYKMCAGWMAWYSWTRTYWMTWMMWASRTAK 996
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1138 ATGAAGTGTGCTPAAGTCAAAAGAGCT 1165
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 997 ARMMWKTBAWSKYARAYWKAAGCACT 1024
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: July 7, 2004, 16:41:45
Job time : 773 secs

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 15:39:14 ; Search time 8003 Seconds

(without alignments)
6878.127 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270
Sequence: 1 gaaagtcgaaggtctctc.....atgaagaaggttacaatca 1270

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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12: gb_sy:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1221.4	96.2	1250	8	AY093009	AY093009 Arabidops
4	1100	86.6	1126	8	BT001192	BT001192 Arabidops
5	529.8	41.7	1142	6	AX034545	AX034545 Sequence
6	518.8	35.6	1396	8	AK065114	AK065114 Oryza sat
7	451.6	35.6	2710	8	ATH224641	AJ224641 Arabidops
8	451.6	35.6	4010	6	AX034541	AX034541 Sequence
9	447.4	35.2	80818	8	AB019232	AB019232 Arabidops
10	229.2	18.0	776	6	AX034547	AX034547 Sequence
11	154	12.1	281	6	AR252083	AR252083 Sequence
12	150.2	11.8	121882	8	AP006144	AP006144 Lotus cor
13	130.4	10.3	135457	8	AC136506	AC136506 Medicago
14	126.6	10.0	123209	8	ATF4F15	AL049711 Arabidops
15	123.2	9.7	125593	8	CNS08CDB	BX004999 Oryza sat
16	116.2	9.1	132703	8	CNS08CDB	AL928756 Oryza sat
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19	86.4	6.8	2341	8	AK073233	AK073233 Oryza sat
20	83.8	6.6	2162	8	AK100844	AK100844 Oryza sat
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24	71	5.6	7218	5	I66494	I66494 Sequence 14
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26	57.6	4.5	207478	2	AC108559	AC108559 Rattus no
27	57.6	4.5	321848	2	AC133831	AC133831 Rattus no
28	57.2	4.5	623	6	AX209863	AX209863 Sequence
29	57.2	4.5	1812	6	AX774794	AX774794 Sequence
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39	53.6	4.2	1448	9	AF141937	AF141937 Actus nan
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ALIGNMENTS

RESULT 1	AX034542	1270 bp	DNA	1linear	PAT 22-SEP-2000
LOCUS	AX034542				
DEFINITION	Sequence 2 from Patent DE19907598.				
ACCESSION	AX034542				
VERSION	AX034542.1	GI:10303140			
KEYWORDS					
SOURCE					
ORGANISM	Arabidopsis thaliana (thale cress)				
	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.				
REFERENCE					
AUTHORS	1				
JOURNAL	Patent: DE 19907598-A 2 24-AUG-2000;				

Pred. No. is the number of results predicted by chance to have a

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Db	61	GATCCAGTCTTCTGAGTACTTCGACGACGACGAGTCACTACTCTTGGACTTCT	120
QY	121	CATACCTTCAACCGAGTTGATTTGGGAATATGATGAAATCTTGGAGATCAAACTCAA	180
Db	121	CATACCTTCAACCGAGTTGATTTGGGAATATGATGAAATCTTGGAGATCAAACTCAA	180
QY	181	ACACATGACCAAGAGGCGAAATAGTTACTGAAGGAAGCGCGTTGTCATAGTGGGCAT	240
Db	181	ACACATGACCAAGAGGCGAAATAGTTACTGAAGGAAGCGCGTTGTCATAGTGGGCAT	240
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Db	241	CTCAAGAGGGTATGTTCTCTCTTAAGTTGATGTAAGTAGAGGTCTTGGATGAGAAAG	300
QY	301	TCAGTAGCAGATTTATTAAGGAAGGTACGCGTTCCAAACCATCCAGTAGTCTTACATGCT	360
Db	301	TCAGTAGCAGATTTATTAAGGAAGGTACGCGTTCCAAACCATCCAGTAGTCTTACATGCT	360
QY	361	TTTGTCATCAACGGGGATGAGACCAAAAATCGGCACACAAATTTGAGGATTCATGGCATG	420
Db	361	TTTGTCATCAACGGGGATGAGACCAAAAATCGGCACACAAATTTGAGGATTCATGGCATG	420
QY	421	AGCAGCAACTATTTGAATTGTTCTTGGAAAAAGAAAAAGAACTACCGGTTTAGCA	480
Db	421	AGCAGCAACTATTTGAATTGTTCTTGGAAAAAGAAAAAGAACTACCGGTTTAGCA	480
QY	481	TGCGTGTGTACATGAAGTCTGCTGAACTGCGCTTGTGCATGTTGGCTGGGAATTAG	540
Db	481	TGCGTGTGTACATGAAGTCTGCTGAACTGCGCTTGTGCATGTTGGCTGGGAATTAG	540
QY	541	CTTATGAGGAAGGAAGAACTTTCTTTTCCCAATGTTCCACTATGGCAACATTTGTTAT	600
Db	541	CTTATGAGGAAGGAAGAACTTTCTTTTCCCAATGTTCCACTATGGAACATTTGTTAT	600
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Db	601	ATGAGGTGAAAGTTATTTGGGTTTGTATGAACAAGAGGGGAAAAAGCTGCGAGTATATGA	660
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QY	721	AGAGAGGAACCTGAGAGAACCTATGCAACAGTATGAATGGCCATAGCATATCATGGGGG	780
Db	721	AGAGAGGAACCTGAGAGAACCTATGCAACAGTATGAATGGCCATAGCATATCATGGGGG	780
QY	781	ACGATTTTATGTTTTCAGCTGTATGCGGAAGTACACAGATATGCGCTTTAGCATTTAAACC	840
Db	781	ACGATTTTATGTTTTCAGCTGTATGCGGAAGTACACAGATATGCGCTTTAGCATTTAAACC	840
QY	841	CATGCCATCTTAAACATAGCAGCTTGCTCATCAAACTTAAACGATACGATACAACTTG	900
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Db	901	GTCTCTGCACACTTGTGTGTGA	CAGAAAGAAAGAAAA	CCAAAAGCACTGTTCCAGAAAG	960
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LOCUS	1360 bp	mRNA	linear	PLN 31-JUL-2000
ATH224640				
DEFINITION	Arabidopsis thaliana mRNA for FKBP-like protein.			
ACCESSION	AJ224640			
VERSION	AJ224640.1	GI:9650630		
KEYWORDS	FKBP gene.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1			
AUTHORS	Kolukisaoglu,U., Berger,U., Eckhoff,A., Moeller,A., Saal,B., Bellini,C. and Schulz,B.			
TITLE	Structure and evolution of FKBP-like genes in Arabidopsis			
JOURNAL	Unpublished			
AUTHORS	2 (bases 1 to 1360)			
TITLE	Schulz,B.			
JOURNAL	Direct Submission			
	Submitted (25-FEB-1998) Schulz B., Max-Debrueck-Laboratory, Max-planck-Institute for Breeding Research, Carl-von-Linne-Weg 10, 50829 Koeln, GERMANY			
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Best Local Similarity 99.7%; Pred. No. 0;
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RESULT 3

AY093009

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AY093009 1250 bp mRNA linear PLN 21-APR-2002
Arabidopsis thaliana FKBP-type peptidyl-prolyl cis-trans
isomerases, putative (At3g21640) mRNA, complete cds.
AY093009.1 GI:20260219
PII CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi-
s (bases 1 to 1250)
Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shimn,P., Yamada,K.,
Shinozaki,K., Ecker,D., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (27-MAR-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA') Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Southwick,A.,
Nguyen,M., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shimn,P.,
Yamada,K., Ecker,D., Theologis,A. and Davis,R.W.

Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PI.

FEATURES

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ORIGIN

Query Match 96.2%; Score 1221.4; DB 8; Length 1250;
Best Local Similarity 99.4%; Pred. No. 6.4e-313;
Matches 1236; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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RESULT 4
BT001192 1126 bp mRNA linear PLN 12-NOV-2002
LOCUS
DEFINITION Arabidopsis thaliana FKBP-type peptidyl-prolyl cis-trans isomerases, putative (At3g21640) mRNA, complete cds.
ACCESSION BT001192
VERSION BT001192.1 GI:24899728
KEYWORDS P1 CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1126)
AUTHORS Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Bann,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shino,M., Yamada,K., Shinzaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: "RIKEN Arabidopsis Full-length cDNA"; Seki,M., Narusaka,M., Ishida,J., Kawai,J., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, RGC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Tripp,M., Southwick,A., Nguyen,M., Palm,C.J., Jones,T., Wu,T., Chen,H., Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,Y.W.,

Lee, J.M., Kim, C.J., Quach, H.L., Shim, P., Tang, C.C., Torount, M.,
Wallender, E.K., Mong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S.,
Ecker, J., Theologis, A. and Davis, R.W.

Trimp, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source

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gene
CDS

ORIGIN

Query Match 86.6%; Score 1100; DB 8; Length 1126;
Best Local Similarity 99.5%; Pred. No. 1.1e-280;

Matches 1114; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 270 GATAGTGAAGTGAAGTCTTGATGAGAAAGTCAAGAGATTAATGAAGAGGTCAC 329
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DB 481 ACNAGAGAGGAAAGTCCGACATGATATGATCTGATGAGAAAGATTTGGTGCACGAC 540
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DB 661 TACGAGATATGCTTTAGCATTTAAAAAACCATGCACTTAACTAGCAGCTGCTC 720
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DB 721 ATCAAACTAAACGATATGATATGAGGAGATTTGCTACTGCAACATTTGTTGACAGAA 780
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DB 781 GAGAAAAAACCAGAAAGCATGTTTCAAGAGGAGAAAGGAGAGAGAGAGAGAGAG 840
QY 990 GACTCAGCAGTATGATTTCCGAAAGGAGCAAAAGATATGCTCTGACAGCAGAGAT 1049
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QY 1230 AGAGTTAAAGCAGATTAATGATGAAGAGGTTTACAAAT 1269
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RESULT 5
AX034545 1142 bp DNA linear PAT 22-SEP-2000

LOCUS AX034545
DEFINITION Sequence 5 from Patent DE19907598.

ACCESSION AX034545
VERSION AX034545.1 GI:10303142

KEYWORDS
SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

AUTHORS
JOURNAL Patent: DE 19907598-A 5 24-AUG-2000;

REFERENCE SCHULZ BURKHARD (DE)

FEATURES
source location/Qualifiers
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ORIGIN

Query Match 41.7%; Score 529.8; DB 6; Length 1142;
Best Local Similarity 73.8%; Pred. No. 2.1e-129;
Matches 666; Conservative 0; Mismatches 242; Indels 1; Gaps 1;
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Db	451	CTGGTTATGAGAAAAGAGAAAAGAAATACATGCGCTACCTATGCGTTAAGCAGATG	510
Qy	498	AAGCTGTGTAACGTCGCTTGTGTCATGTTGGCTGGAAATTAAGCTTATGAGAAAAGAA	557
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Qy	678	GGTGCACAGACAGAAAGAAATGATGAGAAATCTCTTTTAAAGAGAGAACTGGAG	737
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Qy	738	GAAGCCATGCAACGATGTAATGTCATGACATACATGCGGAGACGATTTTATGTTTCA	797
Db	751	GAAGCTATGCAACGATGTAATGTCATGACATATGAGAGATGATCTTATGTTTCA	810
Qy	798	CTGATATGGAAGTACCGAGATATGCGCTTGTGAGCTTAAACCACTCCATCTTAACATA	857
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RESULT 6
 LOCUS AK065114 1396 bp mRNA linear PLN 24-JUL-2003
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J013001006, full insert sequence.
 ACCESSION AK065114
 VERSION AK065114.1 GI:32975132
 KEYWORDS FULL-CDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE	AUTHORS
1	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta, Spermatophyta; Magnoliophyta: Liliopsida, Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
	The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Ooka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Komo, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL	Science 301 (5631), 376-379 (2003)
MEDLINE	22752273
PUBMED	12869764
REFERENCE	2 (bases 1 to 1396)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komo, H., Kouda, M., Koya, S., Kurihara, C., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takeku-Akaike, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
TITLE	Direct Submission
JOURNAL	Submitted (05-DEC-2001) Shohei Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: kikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT	This clone is one of the 28K full-length cDNA clones from japonica rice. URL : http://cdna01.dna.affrc.go.jp/cDNA/ NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M. PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

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LOCUS	Arabidopsis thaliana	genomic DNA,	PLN 27-DEC-2000
ACCESSION	AB019232	BA000014	chromosome 3, pl clone: MIL23.
VERSION	AB019232.1	GI:3869071	
KEYWORDS			
ORGANISM	Arabidopsis thaliana (thale cress)		
REFERENCE	Arabidopsis thaliana		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Spermatophyta; Magnoliophyta, eudicotyledons: core eudicots;		
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
	1 (bases)		
	Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.		
	Structural analysis of Arabidopsis thaliana chromosome 3. I.		
	Sequence features of the regions of 4,504,864 bp covered by sixty		
	PI and TAC clones		
JOURNAL	DNA Res. 7 (2), 131-135 (2000)		
MEDLINE	20277480		
PUBMED	10819329		
REFERENCE	2 (bases 1 to 80818)		
AUTHORS	Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research		
	Institute, Department of Plant Gene Research; 1532-3, Yana,		
	Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,		
	Tel:81-438-52-3935, Fax:81-438-52-3934)		
	Address for correspondence: kaos@kazusa.or.jp		
	For the latest information on annotation of this clone, please see		
	http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MIL23		
	Genes with similarity to proteins in the databases are described in		
	'product' or 'note' qualifiers. Genes that have no significant		
	protein similarity are described as 'unknown protein'.		
	The software programs used to predict genes include: Graal		
	(Informatics Group, Oak Ridge National Laboratory,		
	http://complib.ornl.gov/Graal-1.3/),		
	GENSCAN (S.M. Hebsgaard, et al., CBS, Technical University of		
	Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and		
	SplicePredictor (Volker Brendel, Stanford University,		
	http://gremlini.zool.iastate.edu/cgi-bin/sp.cgi).		
	Genes encoding tRNAs are predicted by tRNAscan-SE		
	(Sean Eddy, Washington University School of Medicine, St. Louis,		
	http://genome.wustl.edu/eddy/tRNAscan-SE/).		
	This sequence may not be the entire insert of this clone. It may be		
	shorter because we remove overlaps between neighboring submissions.		
	The 5' clone is MH09 and the 3' clone is MSD21.		
	Location/Qualifiers		
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FRTGDTHEARAITFYRPARDLVIMNTLIGYAGVNSDDIDAIDAPNNQCGSPDVA
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ISVRVACNSMISCLAIHGKKEALEMFTSMESLDIKPEITFIPLATLIVCHGKPL
EGKRTPEMKTQDVKNPKHAGCLIHLLGSGKKEAYRIVKEMHVPNDVTYIALLG
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transketolase"
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MALPVPVGAASATIPALPFSKSGIGYAAIIEAVGAEETKASVSA"
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KVYFASMAPEYGNALISKMPIKKMVRQIADVDGDRNVLKTVLEIPMGADVNVCTQ
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28322, .28555)
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Query Match 35.2%; Score 447.4; DB 8; Length 80818;
Best local Similarity 69.7%; Pred. No. 1.8e-107;
Matches 830; Conservative 0; Mismatches 21; Indels 340; Gaps 3;
QY 419 TGAGCAGCAACCATGATGCTTCTTGAAAAGAAAAGAACTAGCCGGTTTACG 478
DB 57893 TGTGACTAAGAGTGAATGTTCTGTGACAGAGAAAAGAAAGAACTAGCCGGTTTACG 57834

OY	479	CATGGGTTGCTAGCATGAAAGTGTGGTGAACGCGCTTGTCAGATGTTGGCTGGGAATT	538
Db	57833	CATGGGTGTTGCTAGCATGAAGTGTGGTGAACGCGCTTGTCAGATGTTGGCTGGGAATT	57774
OY	539	AGCTTATGGGAAGAAAGAAACCTTTCTTTTCCCAATGTTCCACCTATGGCAGACTTGT	598
Db	57773	AGCTTATGGGAAGAAAGAAACCTTTCTTTTCCCAATGTTCCACCTATGGCAGACTTGT	57714
OY	599	ATATGAGGTGAAGTATTTGGGTTTGATGAACAAAG-----	636
Db	57713	ATATGAGGTGAAGTATTTGGGTTTGATGAACAAAGAGGTAAATTATTTCTTATACCA	57654
OY	637	-----	636
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OY	637	-----AGGAAAGCTCGCAGTATATGACTGTAGA	667
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OY	668	GGAAGAGATTGTCGACAGACAGAGAAGAAAAATGATGGGAATTCCTTTTAAAGAGGA	727
Db	57533	GGAAGAGATTGTCGACAGACAGAGAAGAAAAATGATGGGAATTCCTTTTAAAGAGGA	57474
OY	728	GAACTCGAGGAACCCATGCACAGTATGAAT-----	760
Db	57473	GAACTCGAGGAACCCATGCACAGTATGAATGAATGTTATGTCATCTCTCTATCTCTATC	57414
OY	761	-----	760
Db	57413	TCTCTTCCAAACATTAAGGTCAAAGTTTAGTTCAGGATCTTAAGTGAAGTCTGTC	57354
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Db	57353	GAGGCTTGTGTGTCTTTCGCGCTTTTGATAGTATGTTTGTGTTTGTTCAGGCCATA	57294
OY	768	GCATTCATGGGGGACGATTTTATGTTTCACTGTATGGAAGATACAGATATAGGCTTTA	827
Db	57293	GCATTCATGGGGGACGATTTTATGTTTCACTGTATGGAAGATACAGATATAGGCTTTA	57234
OY	828	GCAGTTAAAAACCATGCGATCTTAAATAGCAGCTTGCTCATCAACCTAAAGCATAC	887
Db	57233	GCAGTTAAAAACCATGCGATCTTAAATAGCAGCTTGCTCATCAACCTAAAGCATAC	57174
OY	888	GATGAGCAATTGTCACCTGCACATT-----	914
Db	57173	GATGAGCAATTGTCACCTGCACATTGTGAAGCTATCAAAACATTATGGAAGAAA	57114
OY	915	-----GTGT	918
Db	57113	TCATTTAAAGTTCAATCTCGGTTTCTCGAAATCTATCAAACTCAAAACCTTATCAGGTGT	57054
OY	919	TGACAGAAAGAAAGAAAAACCCAAACACCTGTTCAGAAAGGGAAGCAAAAGCGAGAC	978
Db	57053	TGACAGAAAGAAAGAAAAACCCAAACACCTGTTCAGAAAGGGAAGCAAAAGCGAGAC	56994
OY	979	TAGGACAGATGSACTCAGACGTCGTATGTTTCGAAAGGCACAAAGTATGCTCTGAG	1038
Db	56993	TAGGACAGATGSACTCAGACGTCGTATGTTTCGAAAGGCACAAAGTATGCTCTGAG	56934
OY	1039	ACAAAGCGATTGAAGAGAGCTACGAGACCTTGACAGCAGAGAAAGCCTTGTACAA	1098
Db	56933	ACAAAGCGATTGAAGAGAGAGCTACGAGACCTTGACAGCAGAGAAAGCCTTGTACAA	56874
OY	1099	AGCAGAAAGAAATGTACAAAGGAATTTCAAAAGGGAAGATGAAGGTGGCTAAATCAA	1158
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OY	1159	AGAGCCTTTTGTGTTGATGATGTTATGGAATGTTTGTTCCTTTTCTCCGATCT	1218
Db	56813	AGAGCCTTTTGTGTTGATGATGTTATGGAATGTTTGTTCCTTTTCTCCGATCT	56754
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Db	56753	TTCCAGCGCACAAGCTTAACGACATTATATGTATGAAGAAGGTAACATT	56703
RESULT 10			
LOCUS	AX034547/c	776 bp	DNA
DEFINITION	Sequence 7 from Patent DE19907598.		linear
ACCESSION	AX034547		PAT 22-SEP-2000
VERSION	AX034547.1	GI:10303143	
KEYWORDS			
SOURCE			
ORGANISM	Zea mays		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD		
	clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1		
AUTHORS	Patent: DE 19907598-A 7 24-AUG-2000;		
JOURNAL	SCHULZ BORKHARD (DE)		
FEATURES	Location/Qualifiers		
source	1..776	/organism="Zea mays"	
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Query Match	18.0%; Score 229.2; DB 6; Length 776;		
Best Local Similarity	69.2%; Pred. No. 1.2e-49;		
Matches 328; Conservative	0; Mismatches 140; Indels 6; Gaps 1;		
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Db	776 GAGGAGGCCATGCAAGCATATGAATGGCCATTCATACATGGAAGATGATTTATGTTT	717	
Oy	795 CAGCTGATGGAAGTACCAGGATATGGCTTTAGCAGTTAAACCATGCGCATTTAAC	854	
Db	716 CAATTATTTGAAAAGTACAGAGCATGGCTTGCTGTGAAAAATCCATGCGCATCTCAT	657	
Oy	855 ATTAGCAGCTTCCCTCATCAATAAATGAAATGATGAGATGAGCATTTGTCATGCAACTT	914	
Db	656 ATTGCCCGCATGCCGATCAACTTAAGAGATTCATGAGCTATTTGGCGAGTGAAGATT	597	
Oy	915 GTGTTGACAGAAAGAGAAAAACCAAAGCACTGTTACAGAGAGGGAAGCAAGGCA	974	
Db	596 GTTTTGAACAGAAATGAAGTAAATGTCTAAAGCGCTGTTCAGGCGAGGAAAAAGCTAAATCT	537	
Oy	975 GAGCTAGGACAGATGAGACTCAGCACGTGATGATTTCCGAAAAGGCAAAAAGTATGCTCT	1034	
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Db	476 GAAGTCAGAGAGATCATTTGGGAGCTCCGTTTGTCTCGGAAACAAGNACAGGCCCTATAC	417	
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Db	416 CAGAAGCAGAAAGAGCTTACAAAAGTCTTTTGGGCAAGTCTGAA-----GCGAAA	363	
Oy	1155 TCANAAGACCTTTTTTGGTGTATAGTGTATAGCAATGCTTTTCCCCTTTTC	1208	
Db	362 CGAAGAAAGGCAAGTACTCTGTTGTCTTGGGAGTGGCTGAGTCAATTATTC	309	
RESULT 11			
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DEFINITION	Sequence 7442 from patent US 6476212.		linear
ACCESSION	AR252083		PAT 20-DEC-2002
VERSION	AR252083.1	GI:2729957	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		

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gene	

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exon	

Query Match	10.0%;	Score 126.6;	DB 8;	Length 123209;
Best Local Similarity	-77.7%;	Pred. No. 2.4e-22;		
Matches 178; Conservative	0;	Mismatches 49;	Indels 2;	Gaps 2;

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QY	496 TGAAGTCGTGTGACGTGCGCTTGTCATGTTGGCTGGGAA-TTACCTTATGGAAAGAA	554
Db	62827 TCAAGTCGTGTGACGTGCGCTCTTGCAATGTTGCTGGGAAATTAGCATATAGAGAGAT	62768
QY	555 GGAACCTTTTC-TTTTCCCAATGTCACCTATGCGACACTTGTTATATGAGGTGGAAT	613
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QY	614 TATTGGGTTGATGAACAAGAGGGAAGAAAGCTGCACTGATATGACT	662
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RESULT 15

DEFINITION

sativa (rice), complete sequence.

VERSION BX000499.1 GI:25900572

SOURCE

④

AUTHORS

Segurens,B., Pelletier,E., Searpelli,C., Salanoubat,M.,
 Weissenbach,J. and Quetier,F.
 Oryza sativa chromosome 12 sequencing
 JOURNAL
 2 (bases 1 to 125593)
 Unpublished
 Genoscope.
 Direct Submission
 Submitted (09-JAN-2003) Genoscope - Centre National de Sequencage :
 BR 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 On Oct 17, 2003 this sequence version replaced gi:12329146.
 Center: Genoscope / Centre National de Sequencage
 Center code: GS
 Web site: http://www.genoscope.cns.fr/
 Contact: Segref@genoscope.cns.fr

COMMENT

 The following sequence is oriented from the T7 to the SP6 end.

 FINISHED SEGMENT STARTS AT BASE 1
 FINISHED SEGMENT ENDS AT BASE 125593

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 9.7%; Score 123.2; DB 8; Length 125593;
 Best Local Similarity 77.6%; Pred. No. 1.9e-21;
 Matches 149; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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 Db 111744 ACAGAGAAAACCAATGCTGTGTTAGCATGTGTGTACATGAGAGTGGGAG 111803
 QY 510 CGTGCGCTTGTCATGTGGCTGGGAATTAGCTTATGGAAAGGAACTTTCTTTT 569
 Db 111804 CGTGCACTGTGTCATGTGGCTGGGAGCTAGGCTATGGAAAGGAGACTTTTCATTC 111863
 QY 570 CCCAATGTTCCACTATGCGAGACTGTATATGAGGTGAAGTTATGGGTTTGATGAA 629
 Db 111864 CCAATGTCCCTCCAAATGCGAGATCTTTATATGAAGTTGAACCTATTGGGTTTGATGAT 111923
 QY 630 ACAAGAGAGGA 641
 Db 111924 GTCAAAGAGGTA 111935

Search completed: July 7, 2004, 18:55:24
 Job time : 8013 secs

This Page Blank (copy)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 16:22:54 ; Search time 123 Seconds
(without alignments)
5729.981 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270
Sequence: 1 gaaagtcgaagggctctc.....atgaagaaggttacaatca 1270

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCBUS.COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	12.1	281	4	US-09-313-294A-7442
2	71	5.6	7218	1	US-08-232-463-14
3	56.8	4.5	2157	1	US-08-336-618-25
4	56.8	4.5	2246	4	US-09-566-921-48
5	44	3.5	2291	4	US-09-220-132-114
6	40.6	3.2	289	3	US-09-007-005-17
7	40.6	3.2	289	3	US-09-244-796-17
8	39.8	3.1	472	4	US-09-621-976-973
9	37.2	2.9	5252	4	US-09-976-594-308
10	37.2	2.9	5712	4	US-09-976-594-820
11	36.8	2.9	486	3	US-09-358-972-90
12	36.8	2.9	486	4	US-09-406-065-78
13	36.8	2.9	2802	4	US-09-976-594-924
14	36.6	2.9	505	4	US-09-621-976-15639
15	36	2.8	3279	4	US-09-543-681A-2886
16	35.8	2.8	148567	4	US-09-801-876B-3
17	35.8	2.8	148567	4	US-10-254-869-3
18	35.6	2.8	1298	4	US-08-948-705-3
19	35.6	2.8	1298	4	US-09-510-543-3
20	35.4	2.8	1664976	4	US-08-916-421B-1
21	35	2.8	3106	4	US-09-976-594-554
22	34.8	2.7	277	3	US-09-007-005-3
23	34.8	2.7	277	3	US-09-244-796-3
24	34.4	2.7	278	4	US-09-621-976-13872
25	34.4	2.7	603	5	PCT-US92-01691-27
26	34.4	2.7	603	5	PCT-US92-01691-28
27	34.4	2.7	627	4	US-09-833-381-1295

28	34.4	2.7	6519	1	US-08-233-008A-7	Sequence 7, Appl
C 29	34.4	2.7	10993	4	US-08-961-527-15	Sequence 15, Appl
C 30	34.2	2.7	3399	4	US-09-621-976-8976	Sequence 8976, Ap
31	34	2.7	1048	2	US-08-897-340-3	Sequence 3, Appl
32	34	2.7	1048	3	US-09-252-329-3	Sequence 3, Appl
33	34	2.7	1756	2	US-08-879-260-3	Sequence 3, Appl
34	34	2.7	1811	3	US-09-231-529-5	Sequence 5, Appl
35	34	2.7	1811	3	US-08-977-816-5	Sequence 5, Appl
36	33.6	2.6	304	4	US-09-313-294A-7129	Sequence 7129, Ap
37	33.4	2.6	44453	4	US-09-146-053-5	Sequence 5, Appl
38	33.2	2.6	983	3	US-08-960-780-28	Sequence 28, Appl
39	33.2	2.6	983	3	US-09-073-898-28	Sequence 28, Appl
40	33.2	2.6	983	4	US-09-850-351A-28	Sequence 28, Appl
41	33.2	2.6	1069	4	US-09-023-655-166	Sequence 166, App
42	33.2	2.6	1194	3	US-08-860-368B-11	Sequence 11, Appl
43	33.2	2.6	1194	3	US-08-860-368B-11	Sequence 12, Appl
44	33.2	2.6	1641	3	US-08-960-780-22	Sequence 22, Appl
45	33.2	2.6	1641	3	US-09-073-898-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-313-294A-7442

Sequence 7442, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ico, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313, 294A
NUMBER OF SEQ ID NOS: 1999-05-14
SOFTWARE: PERL Program
SEQ ID NO 7442
LENGTH: 281
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inocyte ID No. 6476212 700381733H1
LOCATION: 235
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7442

Query Match 12.1%; Score 154; DB 4; Length 281;

Best Local Similarity 76.4%; Pred. No. 2.6e-37;
Matches 201; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY	642	AAAGCTGCGAGTATGACTGTGAGAGAAAGATTGTCAGACAGACAGAAATAATG	701
DB	2	AAATCCGAGATGACATGACAGTTGAGAGAGATTGCTTCAAGACAGAAAGATT	61
QY	702	GATGGAAATCTCTTTTAAAGAGAGAACTGAGAGAAAGCAATGCAAGATGAAATG	761
DB	62	GAGGGCAATCATATTTTCAAGAAAGAGCTTGAAGAGCCATGCAAGCAATATGAATG	121
QY	762	GCCATGACATACATGCGGAGCAATTTTATGTTTCAGCTGATATGGAAGTACAGATATG	821
DB	122	GCCATTGCAATACATGAGAGATGATTTTCAATTTTATTTGAAAGTACAGACATG	181
QY	822	GCTTTGACAGTTAAACCATGCTTAAATACATGACAGCTTGCTTCAATCAATPAAA	881
DB	182	GCTTGGCTGTGAAAAATCATGCTTCAATATGCTGATGCTTATC-AAATPAAAG	240
QY	882	CGATGACATGACAAATGCTCA	904
DB	241	AGATTGATGAAATGCTTATGCGCA	263

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RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1600 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match          5.6%; Score 71; DB 1; Length 7218;
Best Local Similarity 3.6%; Pred. No. 4,2e-11;
Matches 14; Conservative 236; Mismatches 141; Indels 0; Gaps 0;

QY      601 ATGAGGTGAAGTATTGGCTTGATGTAACAAAGAAGGAAAAGCTCGCATGATATGA 660
       ||| |||| |||| : : : : : : : : : : : : : : : : : : : : : :
Db      1456 AAGAGTAGAAGAAATTGGTCACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1397

QY      661 CTGTAGAGGAAGAAGATTGGTCACAGACAAGAAAAAATGATGGCAATCTTTT 720
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1396 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1337

QY      721 AGAGAGGAAACTGAGAGAACCCATGCATAAGTAAATGCCATAGCATATCGGGG 780
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1336 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1277

QY      781 ACAGATTTTATGTTCAAGCTGTATGGGAAGTACCAGATATGCTTTAGCAGTTAAAA 840
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1276 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1217

QY      841 CATGCCATCTTAATAGTACGAGCTTGCTCATCAAACTAAACGATAGCATAAACAATTG 900
       : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1216 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1157

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Oy      901 GTACGACGACATGTGTTGACACAGAGAAGAAAAACCCAAAGACATCTGCAGAGAG 960
Db      1156 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1097
Oy      961 GGAAGCGAAGACGACGACTGACAGACATGCA 991
Db      1096 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRA 1066

RESULT 3
US-08-336-618-25
: Sequence 25, Application US/08336618
: Patent No. 5763590
: GENERAL INFORMATION:
: APPLICANT: Peattie, Debra A.
: APPLICANT: Harding, Matthew W.
: APPLICANT: Livingston, David J.
: TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
: TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
: TITLE OF INVENTION: CDNA
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/336,618
: FILING DATE: 09-NOV-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/963,325
: FILING DATE: 16-OCT-1992
: APPLICATION NUMBER: US 07/777,752
: FILING DATE: 11-OCT-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Granahan, Patricia
: REGISTRATION NUMBER: 32,227
: REFERENCE/DOCKET NUMBER: VP191-06A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-6240
: TELEFAX: 617-861-9540
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2157 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 100..1476
: US-08-336-618-25

Query Match 4.5%; Score 56.8; DB 1; Length 2157;
Best Local Similarity 47.5%; Pred. No. 4.6e-07;
Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

471 GGTTCGCATGGGTGTGCTGACATGAAGTCTGGGAAACGCGCTTGTCATGTTGGC 530
706 GGCTCTGAAGAGGCCATTGACGCGCATGGAGAAAGAACATTTTCATCTGTGTAAG 765

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Qy 531 TGGGAATTAGCTTATGGGAAGAAGAACTTTCTTCCCAATGTTCCACCTATGCA 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 766 CCACGATATGCTTTGGCAGTGTGGAGAGAAAGTT-----CMAATCCCAACCAATGCT 822
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 591 GACTTGTATATAGAGTGAAGTATATGGGTTTGATGAAACAAAGAGAGAAAGCTGCG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 823 GAGCTGAAATATGATTTACACCTCAAGAGTTTGGAAAGGCCAAGAG-----TCT 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 651 AGTATATGACTGTAGAGAAAGATTGTGTGACAGACAGAGAAAGAAATGATGGCAT 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 TGGAGATGATTCAGAGAGAGAGCTGAAACAGACACATATGAAAGAGCGGGGCACT 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 711 TCTCTTTTAAAGAGAGAACTGGAGAGCCATGCAAGTATGAAATGGCCATGCA 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 GTGTACTCAAGAGAGTAAATACAGCAAGCTTTACTACAGTATAGAAAGATGTGTCT 993
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 771 TACATGGGGACGATTTTATGTTTCACTGTATGGAGTACAGATATGGCTTTAGCA 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 994 TGGCTGGAATATGATGCTAGTTTT-----TCCAATGAGAGACAGAAAGCAGGCC 1047
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 831 GTTAAACCCATGCACTTTTACATAGCAGCTTGCTCATCAACTTAAACGATACAT 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1048 CTTCGACTGGCTCTCACTCAACCTGGCCATGTGTATGTAAACTACAGGCTTCTCT 1107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 891 GAGCAATTGCTCATGCAACATTTGTGTGACAGAAAGAGAAACCCAAAGACACTG 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1108 GTGCCATTGAAAGCTTTAACAGAGCCCTAGAACTGACAGCAACAGAGAGGCTCT 1167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 951 TTCAAGAGAGAGAAAGCAAGAGCAGAGCTAGACAGATGACCTGACAGCTGATTTTC 1010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1168 TTCCGCCGGGAGAGGCCCACTGGCCGTGAATGACTTTGAACGAGACGGGCTGATTTCT 1227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1011 CGAAGGACAAAGATATGCTCTCTGACGACAGGCGCATTTAGAGAGACT 1060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1228 CAGAAAGTCTCTGACGCTCTACCCCAACAGAAAGCCCAAGACCCAGCT 1277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 4
US-09-566-921-48
; Sequence 48, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla W.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 2246
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6682888 474194.5
US-09-566-921-48

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Query Match 4.5%; Score 56.8; DB 4; Length 2246;
Best Local Similarity 47.5%; Pred. No. 4.7e-07;
Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;
Qy 471 GGTTCACATCGGTTGCTAGCATGATCTGTAAAGTGGCTTGTGATGTTGGC 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 GGTTCAGAGAGGCGCATTTACGCGATGAGAAAGAAACATTCATCGTGTACTCAAG 821
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 531 TGGGAATTAAGCTTATGAGAAAGAAAGAACTTTTCCCAATGTTCCACTATGCA 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 822 CCCAGCTATGCTTTGGCAAGTGTGGAGAAAGAAAGTT---CCAATCCCAACCAATGCT 878
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 591 GACTTGTATATGAGTGAAGTATTTGGTTTATGAAACAAAGAGAGGAAAGCTGCG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 879 GAGCTGAATATGATTTACACCTCAAGAGTTTGGAAAGGCCAAGAG-----TCT 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 651 AGTATATGACTGTAGAGAAAGATTGTGTGACAGACAGAAAGAAATGATGGCAAT 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 930 TGGAGATGAAATTCAGAAAGAAAGCTGGAACAGACACCATATGTGAAGAGCGGGCAGCT 989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 711 TCTCTTTTAAAGAGAGAACTGGAGAGCCATGCAACAGTATGAAATGGCCATAGCA 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 990 GTGTACTCAAGAGAGTAAATACAGCAAGCTTTACTACAGTATAGAAAGATGTGTCT 1049
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 771 TACATGGGGACGATTTTATGTTTCACTGTATGGAGTACAGGATATGCTTTAGCA 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1050 TGGCTGGAATATGATGCTAGTTTT-----TCCAATGAGAGACAGAAAGCAGGCC 1103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 831 GTTAAACCCATGCACTTTTACATAGCAGCTTGCTCATCAACTTAAACGATACAT 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1104 CTTCGACTGGCTCTCACTCAACCTGGCCATGTGTATCTGAACTACAGGCTTCTCT 1163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 891 GAGCAATTGCTCATGCAACATTTGTGTGACAGAAAGAGAAACCCAAAGACACTG 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1164 GTGCCATTGAAAGCTTTAACAGAGCCCTAGAACTGGAACAGCAACAGAGAGGCTCT 1223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 951 TTCAAGAGAGAGAAAGCAAGAGCAGAGCTAGACAGATGGAATCAGCAGCTGATTTTC 1010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1224 TTCCGCCGGGAGAGGCCCACTGGCCGTGAATGACTTTGAATGAGCAGCGGCTGATTTCT 1283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1011 CGAAGGACAAAGATATGCTCTCTGACGACAGGCGCATTTAGAGAGACT 1060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1284 CAGAAAGTCTCTGACGCTCTACCCCAACAGAAAGCCCAAGACCCAGCT 1333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 5
US-09-220-132-114
; Sequence 114, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; FILE REFERENCE: 0734-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 2291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-114

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Query Match 3.5%; Score 44; DB 4; Length 2291;
Best Local Similarity 45.8%; Pred. No. 0.0039;
Matches 281; Conservative 0; Mismatches 315; Indels 18; Gaps 3;
Qy 447 GGAAGAGAGAAAGAAAGAACTAGCGGTTTACGATCGGTGTTCTGATGAAGTCTGCT 506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 554 GGAAGAGACCAACACATTCATATTTGAATTTGACAAAGCTGTGAGAAATATGACGGGAA 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 507 GAACTGCGCTTGTGATGATGTTGCTGGAAATTAGCTTATGGAAGAAAGAACTTTTCT 566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 614 GAACATATATTTTATATCTTTGACCAAGATATGTTTGGAGAGCAAGGAAAGCTTAA 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 567 TTTCCTCAATGTTTCACTTATGAGCACTGTATATAGAGTGAAGTATATGAGTTGAT 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 674 TTTCGCA---TTAACCTAATGCTGAGCTTATATATGAAGTTTACCTTAAAGCTTCG-- 728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 627 GAAACAAAGAGGAAAGCTGCAAGTATATGATGATGATGAGAAAGAAAGTTGGTGCAGCA 686
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Db 729 -----AAAGGCCAAAGAAATCTGGAGATGATACCAAGAAATAATTTGAGACAGCT 781
Qy 687 GACAGAGAAATAATGATGGAAATCTCTTTTAAAGAGAGAAACTGGAGAAAGCATG 746
Db 782 GCCATTGTCAAGAGAGAGGAAACGTAATCTTCAAGGAGGCAAAATACATGACAGCGGTG 841
Qy 747 CAACAGATGATAATGCGCATAGCATATGAGGAGGACATTTTATGTTTACGTATGAG 806
Db 842 ATTCAATATGGGAAGATAGTGTCTGTTAGAGATGAAATATGTT-----TATCGAA 895
Qy 807 AAGTACCAAGATATGCTTTAGACGTTAAAAACCATGCATCTTAAATACAGACGCTTC 866
Db 896 AAGGAATCGAAAGCTTCTGAATCATTTCTCTGCTCTCTTTCGAAACCTGGCCATGTC 955
Qy 867 CTATCAACTAAAGCATACGATGAGCAATTTGTCATCGCAACATTTGTTGACAGAA 926
Db 956 TACTTGAAGCTTAAAGAAATACCAAGAGCTGTGTAATGCTGTGCAAGGCCCTTGAGCTG 1015
Qy 927 GAAGAGAAAAACCCAAAGACATGTTCAAGAGAGGAGCAAAAGGACGAGCTAGACAG 986
Db 1016 GACAGTCCCAATGAGAAAGGCTGTATAGAGAGGGGTGAAGCCAGCTGCTCATGAAAGAG 1075
Qy 987 ATGACTCAGACGCTGATGATTTCCGAAAGGACAAAGATATGCTCTTGAACGACAGCG 1046
Db 1076 TTGAGTCAGCAAGGCTGACTTTGAGAAAGTCTGGAAGTAAACCCCAATATAGGCT 1135
Qy 1047 ATTGAAGAGAGCT 1060
Db 1136 GCAGACTGCAGAT 1149

RESULT 6

US-09-007-005-17
Sequence 17, Application US/0907005B
Patent No. 6258558
GENERAL INFORMATION:
APPLICANT: Szoestak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihc
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007, 005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035, 963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064, 491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match 3.2%, Score 40.6; DB 3; Length 289;
Best Local Similarity 6.2%; Pred. No. 0.013;
Matches 16; Conservative 122; Mismatches 117; Indels 3; Gaps 1;
Qy 907 GCAACATTGTGTGACAGAGAGAGAAAGAAACCCAAAGCACTGTTCAGAGAGGAAAG 966
Db 9 RCRARARURARCRURARURURARCRARARURARURARURARURARURARURARURAR 68
Qy 967 CAAAGCAGAGCTAGCAGATGACATCAGACGCTGATGATTTCCGAAAGGACAAAGT 1026
Db 69 RNR 128

Qy 1027 ATGCTCCTGACGACAGGAGATTAGAGAGAGCTACAGACCTTGCGAGAGCAAGAAAG 1086
Db 129 RNR 188
Qy 1087 CCTTGTAC---CAAAGCAGAAAGAAATGTACAAAGAAATATTCAAAGGAGAAAGATGAG 1143
Db 189 RNR 248
Qy 1144 GTGCTGCTAAGTCAAGA 1161
Db 249 RNRGRGRGRUAAAAA 266

RESULT 7

US-09-244-796-17
Sequence 17, Application US/09244796
Patent No. 6281344
GENERAL INFORMATION:
APPLICANT: Szoestak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihc
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244, 796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035, 963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064, 491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007, 005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match 3.2%, Score 40.6; DB 3; Length 289;
Best Local Similarity 6.2%; Pred. No. 0.013;
Matches 16; Conservative 122; Mismatches 117; Indels 3; Gaps 1;

Qy 907 GCAACATTGTGTGACAGAGAGAGAAAGAAACCCAAAGCACTGTTCAGAGAGGAAAG 966
Db 9 RCRARARURARCRURARURURARCRARARURARURARURARURARURARURARURAR 68
Qy 967 CAAAGCAGAGCTAGCAGATGACACTCAGACGCTGATGATTTCCGAAAGGACAAAGT 1026
Db 69 RNR 128
Qy 1027 ATGCTCCTGACGACAGGAGGATTTAGAGAGAGCTACAGACCTTGCGAGAGCAAGAAAG 1086
Db 129 RNR 188
Qy 1087 CCTTGTAC---CAAAGCAGAAAGAAATGTACAAAGAAATATTCAAAGGAGAAAGATGAG 1143
Db 189 RNR 248
Qy 1144 GTGCTGCTAAGTCAAGA 1161
Db 249 RNRGRGRGRUAAAAA 266

RESULT 8

US-09-621-976-973
; Sequence 973, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; PRIORITY FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 973
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..471
US-09-621-976-973

Query Match 3.1%; Score 39.8; DB 4; Length 472;
Best Local Similarity 50.8%; Pred. No. 0.031;
Matches 95; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 158 AATCTCTGGAGCATCAAACTCAACACATGACCAAGAGCGAAATGTTACTGAAGAA 217
DB 268 AAGGCCAGATGAAAAAGCTCCGAGAGAGAGCCAGATAGAGTACCGCTGAGTAC 327
QY 218 GTGCGCTTGTGATAGTGGCATCTCAAGAGGGTAATGTTCTCCCTAAAGTTAGTGA 277
DB 328 CTGCGGCTGGCGCAAGGCGCCAGCCAGCTGTTTAAATGCTGTAATTTGTGATGA 387
QY 278 AGCTGAGCTTTCGATGAGAAAGTCACTAAGCAGATTATTAAGAGAGCTGACCGTTCCAA 337
DB 388 ATGCTGCTGCTTGAAGAAATTTCTTAAGCAAAAAGAAAGAGTACTTGCTTAAG 447
QY 338 ACCATCC 344
DB 448 AAGCTCC 454

RESULT 9
US-09-976-594-308
; Sequence 308, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976.594
; PRIORITY FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIORITY FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 308
; LENGTH: 5252
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2619838C81
US-09-976-594-308

Query Match 2.9%; Score 37.2; DB 4; Length 5252;
Best Local Similarity 51.2%; Pred. No. 0.76; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 870 ATCAAACTAAAGCATGATGAAAGCAATGCTCACTGCAACATGCTTGAAGAGAA 929

DB 303 ATCAGAAACAAAGATATCAAGAGCTTTGAACAACCTGTAGACAGTGTAAAGCAAG 362
QY 1930 GAGAAACCCAAAGCACTGTTTCAGAGAGGAAAGCAAGCAGAGTACAGACAG 989
DB 363 AAAAATATCTATATATCTGCGGTTTTTATTTGGCGTTGCGAGCTGAACCTAAGCAACT 422
QY 990 GACTCAGCAGTGATGATTTCCGAAAGGCAAAAGATATGCTCTGACGA 1039
DB 423 GATCAGGCCCAAGTGCTCTATATAAAAGCTGCTGAATTAGACCAAGACCA 472

RESULT 10
US-09-976-594-820
; Sequence 820, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976.594
; PRIORITY FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIORITY FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 820
; LENGTH: 5712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 427967.4
US-09-976-594-820

Query Match 2.9%; Score 37.2; DB 4; Length 5712;
Best Local Similarity 51.2%; Pred. No. 0.8;
Matches 87; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 870 ATCAAACTAAAGATATCAAGAGCTTTGCTCACTGCAACATTTGTTGACAGAA 929
DB 339 ATCAGAAACAAAGATATCAAGAGCTTTGAAACACTGTATGAAAGCAAGCAAG 398
QY 930 GAGAAACCCAAAGCACTGTTTCAGAGAGGAAAGCAAGCAGAGTACAGACAG 989
DB 399 AAAAATATCTATATATCTGCGGTTTTTATTTGGCGTTGCGAGCTGAACCTAAGCAACT 458
QY 990 GACTCAGCAGTGATGATTTCCGAAAGGCAAAAGATATGCTCTGACGA 1039
DB 459 GATCAGGCCCAAGTGCTCTATATAAAAGCTGCTGAATTAGACCAAGACCA 508

RESULT 11
US-09-358-972-90
; Sequence 90, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W.
; APPLICANT: Lewis, Martin K.
; APPLICANT: Liepke, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/358.972
; PRIORITY FILING DATE: 1999-07-22

EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 486
TYPE: DNA
ORGANISM: Pyrococcus furiosus
US-09-358-972-90

Query Match 2.9%; Score 36.8; DB 3; Length 486;
Best Local Similarity 56.7%; Pred. No. 0.26;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 653 TGATATGCTGTAGAGAAAGATTGGTGCAGACAGAAAGAAATGGATGGAAATTC 712
DB 222 TGTATGCTGTGAGGAAAGTATGCAAGTATGAAAGATGGCTGGAGCTAC 281
QY 713 TCTTTTAAGAGAGAACTGAGAGCCATGCCATGCAATGCAATGCGCATAGCATA 772
DB 282 TGATCCAAAGACGACAGCAGCTGGACATTTAGGGAGATTATGACTTGACATAGGAGA 341

RESULT 12

US-09-406-065-78
Sequence 78, Application US/09406065
Patent No. 6312902
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Leippe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kepnart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Improved Nucleic Acid Detection
FILE REFERENCE: Improved Nucleic Acid Detection
CURRENT APPLICATION NUMBER: US/09/406,065
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 09/358,972
EARLIER FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 78
LENGTH: 486
TYPE: DNA
ORGANISM: Pyrococcus furiosus
US-09-406-065-78

Query Match 2.9%; Score 36.8; DB 4; Length 486;
Best Local Similarity 56.7%; Pred. No. 0.26;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 653 TGATATGCTGTAGAGAAAGATTGGTGCAGACAGAAAGAAATGGATGGAAATTC 712
DB 222 TGTATGCTGTGAGGAAAGTATGCAAGTATGAAAGATGGCTGGAGCTAC 281
QY 713 TCTTTTAAGAGAGAACTGAGAGCCATGCCATGCAATGCAATGCGCATAGCATA 772
DB 282 TGATCCAAAGACGACAGCAGCTGGACATTTAGGGAGATTATGACTTGACATAGGAGA 341

RESULT 13

US-09-976-594-924
Sequence 924, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 924
LENGTH: 2802
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 481118.7
NAME/KEY: unsure
LOCATION: 1873, 2029
OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-924

Query Match 2.9%; Score 36.8; DB 4; Length 2802;
Best Local Similarity 47.1%; Pred. No. 0.7; 162; Indels 3; Gaps 1;
Matches 147; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

QY 848 TCTTAACATAGACAGCTTGCCTCATCAACTAAACGATGATGAGCAATTGGTCATCG 907
DB 1006 TGTGAAGATCGAGGTGATGATTTTAAAGTTGGAGCCATGAGATGATGAATAA 1065
QY 908 CAACATTGTTGTCAGAGAAAGAAACCAAAAGCATGTTTCAAGAGGAAAGC 967
DB 1066 CATAAAGCTTTTGAATATGACAAACGTAAGCTTTGTAAGCTTGGAGACATT 1125
QY 968 AAGGACAGAGCTAGGACAGATGAGCTCAGACGTGATGATTTCCGAAAGGCAC--AAA 1024
DB 1126 ATATGCGACAAAGGAAGTTTGAACAAAGCATAGAGATTTTGAAGCTTGCTTAGA 1185
QY 1025 GTATGCTCTGACGACAGAGCGATTAGAAAGAGCTACGACCTTGACAGCAAGAGA 1084
DB 1186 CTGTCACTCAGAGAAATGCAAGAAATACCTCTGCGACACCTGTAGAGAGGAGG 1245
QY 1085 AGCTTGTACCAAGACGAAAGAAATGTACAAAGAAATTTCAAGGAAAGATGAGG 1144
DB 1246 ACAGTTAGAAAGAAAGAAAGTTTAAATGCTGAAGTTACTATMAAGAAAGCTTTGGC 1305
QY 1145 TGGTGCTAAGTC 1156
DB 1306 TTGTGATGAGAC 1317

RESULT 14

US-09-621-976-15639/C
Sequence 15639, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Joubert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15639
LENGTH: 505
TYPE: DNA
ORGANISM: Homo sapiens

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 18:55:30 ; Search time 829 Seconds
(without alignments)
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Title:	US-09-914-220B-2
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:  6326084
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
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Published Applications NA:*

- 1: /cgn2_6/prodatae/1/pubnpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/prodatae/1/pubnpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/prodatae/1/pubnpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodatae/1/pubnpna/US06_PUBCOMB.seq.*
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- 8: /cgn2_6/prodatae/1/pubnpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/prodatae/1/pubnpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/prodatae/1/pubnpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/prodatae/1/pubnpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/prodatae/1/pubnpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/prodatae/1/pubnpna/US09_NEW_PUB.seq2
- 14: /cgn2_6/prodatae/1/pubnpna/US10A_PUBCOMB.seq
- 15: /cgn2_6/prodatae/1/pubnpna/US10B_PUBCOMB.seq
- 16: /cgn2_6/prodatae/1/pubnpna/US10C_PUBCOMB.seq
- 17: /cgn2_6/prodatae/1/pubnpna/US10_NEW_PUB.seq
- 18: /cgn2_6/prodatae/1/pubnpna/US10_NEW_PUB.seq
- 19: /cgn2_6/prodatae/1/pubnpna/US60_PUBCOMB.seq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	533.4	42.0	1673	13	US-10-424-569-138705	Sequence 1879.5, App
c	510.2	40.2	1699	17	US-10-437-766-82511	Sequence 8251.1, App
3	486.8	38.3	1432	13	US-10-425-114-26760	Sequence 2676.0, App
4	463.8	36.5	1082	16	US-10-425-114-1944-19	Sequence 19, App
5	372.2	29.3	902	13	US-10-425-114-29666	Sequence 2966.6, App
6	298.8	23.5	864	16	US-10-259-194A-584	Sequence 584, App
7	254	20.0	376	12	US-09-732-627A-1173	Sequence 1173, App
c	8	252	469	16	US-10-259-194A-460	Sequence 460, App
9	210.4	16.6	1458	13	US-10-424-599-138708	Sequence 13870.8, App
10	204.4	16.1	602	17	US-10-437-963-88914	Sequence 8891.4, App
11	126.6	10.0	968	9	US-09-770-445-291	Sequence 291, App
12	103.6	8.2	1171	13	US-10-425-114-34860	Sequence 3486.0, App
13	103.6	8.2	2019	16	US-10-310-154-126	Sequence 126, App
14	102.8	8.1	1617	13	US-10-425-114-13768	Sequence 1376.8, App

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15 96.6 7.6 2566 13 US-10-424-599-31694 Sequence 31694, A
16 86.4 6.8 854 13 US-10-425-114-35161 Sequence 35161, A
17 84.2 6.6 1241 16 US-10-260-238-4097 Sequence 4097, Ap
18 83.8 6.6 2184 17 US-10-437-963-55530 Sequence 55530, A
19 80 6.3 926 17 US-10-437-963-18428 Sequence 18428, A
20 79.6 6.3 843 13 US-10-424-599-138706 Sequence 138706, A
21 76.4 6.0 2045 13 US-10-424-599-91131 Sequence 91131, A
22 73 5.7 2835 13 US-10-424-599-17160 Sequence 17160, A
23 70 5.5 3387 13 US-10-424-599-80948 Sequence 80948, A
24 66.4 5.2 743 13 US-10-425-114-13415 Sequence 13415, A
25 65.8 5.1 412 13 US-10-425-114-23635 Sequence 23635, A
26 64.8 5.2 728 12 US-09-732-6278-3203 Sequence 3203, Ap
27 60.4 4.8 1727 16 US-10-260-238-488 Sequence 488, App
28 57.2 4.5 623 9 US-09-777-564-1703 Sequence 1703, Ap
29 57.2 4.5 623 15 US-10-015-219-1703 Sequence 1703, Ap
30 57.2 4.5 1812 17 US-10-283-9758-1110 Sequence 110, App
31 56.8 4.5 1903 13 US-09-925-298-27 Sequence 27, Appl
32 56.8 4.5 1903 15 US-10-102-808-27 Sequence 27, Appl
33 56.8 4.5 2156 15 US-10-177-293-139 Sequence 139, App
34 56.8 4.5 2246 15 US-10-101-510-428 Sequence 428, App
35 54.4 4.3 360 12 US-09-732-6278-1672 Sequence 1672, Ap
36 53 4.2 2254 17 US-10-437-963-27221 Sequence 27221, A
37 52.8 4.2 2520 17 US-10-437-963-27220 Sequence 27220, A
38 52.6 4.1 2360 17 US-10-437-963-18427 Sequence 18427, A
39 51.2 4.0 641 13 US-10-424-599-80123 Sequence 80123, A
40 50.2 4.0 3387 13 US-10-424-599-80948 Sequence 80948, A
41 49.2 3.9 1002 17 US-10-437-963-9261 Sequence 9261, Ap
42 49 3.9 769 13 US-10-424-599-124540 Sequence 124540,
43 48 3.8 2040 13 US-10-424-599-130000 Sequence 130000,
44 47.2 3.7 513509 10 US-09-754-8534-4 Sequence 4, Appl
45 46.6 3.7 2031 17 US-10-437-963-81510 Sequence 81510, A

ALIGNMENTS

RESULT 1
US-10-424-599-138705
; Sequence 138705, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(513223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 138705
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96258C.1
US-10-424-599-138705

Query Match 42.0%; Score 533.4; DB 13; Length 1673;
Best Local Similarity 68.9%; Pred. No. 7e-149;
Matches 765; Conservative 0; Mismatches 336; Indels 10; Gaps 2;

144 GGAATATATGATTAATCTCTGAGATCAACATCAACAATGACCAAGAGCGAAAT 203
186 GGAGAAAGTTCAAGAGCTCTCAAAACCAATCATCTCCCTGGCTCAGAAAGAAATGTAAGT 245
204 AGTACTGAAGGAAGTCCGTTGTGCATAGTG---GCCATTTCAAGAGGTAATGTTCC 259
246 GATTACTGAAGAGTTCAAGCATTTGTTAAGGGGGAACCGGACACAGAAATTCAGTGAACCC 305
260 TCCTAAGGTGATGTGAAGCTGAGGCTTGAGATGANAAGTCAAGTAAGCAAGATTATTA 319

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Db 306 CCAAAAGTTGATCTGAAAGTTGAGTCTTCATGAGAGGTGAGCAAAACAAATCATTTAA 365
Qy 320 GGAAGTCAGCGTTCCTCAACCATCAATCTTACATGCTTTTGTCACTACAGGGATG 379
Db 366 GGAAGTCATAGCCAGAAACCTTCCAAATATTTCACTTCTTCCATTTACAGGGGCTG 425
Qy 380 GACCAAAAATCTCGAGCACAATTTGAGATACATGAGTACAGAGCACTTATTAAT 439
Db 426 GGTGAGAAATCAACAACAAATTTGAGACATGAGAGAGCAAGGCAATTTGAT 485
Qy 440 GGTCTTGAGAAAAGAAAAAGAACTAGCCGTTTACCATCGTGTGTCAGATGA 499
Db 486 GGTCTTGAGAAAAGAAAAAGAAATGACTGGGTTGGGCAATTTGCTGGCAGCAATGA 545
Qy 500 GTCTGTGAAAGTGTGCTGTGTCAGATGTTGCTGGGAAATTTAGCTATAGGAAAGAA 559
Db 546 AGCTGGGAGCGGGCGTTGGTGTGCTGTGCGGCTGGGAAATTTAGATATGAGAGAGAG 605
Qy 560 CTTTCTTTTCCCAATGTTCCACCTATGAGCACTTGTATATAGAGTGAAGTTATGG 619
Db 606 CTTCTCTTTTCCAAATGTTCCACCAAGGAGATTTAGTTTATGAGTTGAGCTCATTTGG 665
Qy 620 GTTGTATGAAACAAAGAGGAGAAAGCTCGCATGATATGACTGTAGAGAGAAAGATTGG 679
Db 666 CTTTGTATGAAACCAAGAGGCAAGCTCGCATGATATGACTGTGAGAGAAAGAAATTTGG 725
Qy 680 TGCAGACAGACAGAGAAAAATGATGGGAATTTCTTTTTPAAGAGAGAAATCGAGAG 739
Db 726 TGCAGACAGACCGAGAAAGATGATGAAATGCTTTGTATCGAGAGAAAGAAATCGAGAG 785
Qy 740 AGCATGCAACAGATGAAATGGCCATGATACATGAGGAGAGCAATTTATGTTTCAGCT 799
Db 786 GGTATGCAACAGATGAAATGGCCATGATATGAGAGATGATCTTCATGTTCCAGGG 845
Qy 800 GTATGGAGATGACAGATATGCTTTAGCAGTTAAAAACCATGCTCATTAACATAGC 859
Db 846 CTGGAGAAAGACGAGAGGGGGCTCTGGCAGTAAAGATTCATGCCATCTTAAACATAGC 905
Qy 860 AGCTTGCTCTCAATCAAACTAAACATGATGAGTAAAGCAATTTGCTCAACATTTGCTT 919
Db 906 AGCTTGTTGATTTAGCTGAACCTTACGAGAGAGCCATGAGACATGAGCAGCTTTGACT 965
Qy 920 GACAGAAAGAGAAAAACCAAAAGCACTGTTCAAGAGAGGAGCAAAAGCAGAGCT 979
Db 966 GGGGAGAGATGAGAAACATGAGAGCATTTATTTAGCGAGGTAAAGCTAGAGAGAGACT 1025
Qy 980 AGCATGATGACTCAGACAGCTGATGATTTCCGAAAGGCAAAAGATATCTCTTGACGA 1039
Db 1026 TGGGCAAAACGATATCTCCAGAGGAAATTTCTTAAAGGCAAGTAAATATGCCCTCAAGA 1085
Qy 1040 CAAGGCAATTAAGAGAGACTACGAGACTTGACAGCAAGAGAAAGCTTTGTACAAA 1099
Db 1086 CAAGGCAATTTCTAAAGATTTGAGATTTGCTTGTGCAACATGACAGAGCTGTTTACAAA 1145
Qy 1100 GCAGAAAGAAATGTACAAAGAAATTTCAAGGAGAAAGATGAGAGTGTGCTAAGTCAA 1159
Db 1146 GCAGAAAGAAATATATTAAGAAATTTGACCAAGGCTCAACAGATTTCTTAAAGCAAG 1205
Qy 1160 GAGCTTTTGTGTTGATATGTTATGAGCAATGTTTCCCTTTTCCCTGATCTT 1219
Db 1206 AA-----ATTGGCTCAATCTTATTTGGCAGTGTGCTTTCAGTATTTATGAGCTTGT 1259
Qy 1220 TCGAGCGCACAGATTAAGAGATTAATCT 1250
Db 1260 CAGCTCTTCAAGGCTCAAGGCAATAATCT 1290
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RESULT 2

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US-10-437-963-82511/c
; Sequence 82511, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
```

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82511
; LENGTH: 1699
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81934C.1
US-10-437-963-82511
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Query Match 40.2%; Score 510.2; DB 17; Length 1699;

Best Local Similarity 72.3%; Pred. No. 6.6e-142; Mismatches 258; Indels 1; Gaps 1;

Matches 676; Conservative 0; Mismatches 258; Indels 1; Gaps 1;

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Qy 193 GAGAGCAAAATAGTTACTGAGAGAGAGTGGCGTTGTGATATG-GCCATCTCAAGAGGT 251
Db 1410 GATATAGAGATTAAGTATGAGAGAGAGTCTTTTGTGATATGAACTCCGCAAGATGGC 1351
Qy 252 AATGTTCTCTTAAAGTTGATGATGAGTGAAGTCTTGGATGAGAAAGTCAAGTACAG 311
Db 1350 TCTGTCCACCTGTGTTCTCTTAATATGAGAGTCTTCAATGACAAAGTTAAACAA 1291
Qy 312 ATTATAGAGAGAGTACCGTTCCAAACCATCCAACTACTCAATGCTTTTGTGACTAC 371
Db 1290 GTATCAAAAGAGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1231
Qy 372 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
Db 1230 AGAGCTTGGGTTCAAGGCTCTGCAATTAATGAGATATCTTGGAGAGAGAGAGAGAG 1171
Qy 432 ATTGAATTTGTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
Db 1170 ATTGAATTTGTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1111
Qy 492 AGCATGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
Db 1110 AACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1051
Qy 552 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611
Db 1050 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 991
Qy 612 GTTATTTGGGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
Db 990 CTTATTTGGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
Qy 672 AGGATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
Db 930 AGGATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 871
Qy 732 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
Db 870 TTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
Qy 792 TTTCACTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
Db 810 TTTCAATTTGTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
Qy 852 AACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911
Db 750 AACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691
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QY	912	ATTGTTGTCACGAAGAAGAAAAA	CCAAAAAGCACTGTTCAAGAGGAAAAAGCAAG	971
DB	650	ATTGTTGTCACGAAGATAAAA <td>CAATGTGAAGCACTGTTCAAGAGGAAAAAGCAAG</td> <td>631</td>	CAATGTGAAGCACTGTTCAAGAGGAAAAAGCAAG	631
QY	972	GCAAGACTAGACAGATGAGACT <td>CAAGCACTGATTTTCCGAAGGCAAAAAGTATGCT</td> <td>1031</td>	CAAGCACTGATTTTCCGAAGGCAAAAAGTATGCT	1031
DB	630	GCTGAACCTTGTCACAGCA <td>CAATTCAGAGGAGGAGGACTTCTGTAAGCCAAAGAAACATTC</td> <td>571</td>	CAATTCAGAGGAGGAGGACTTCTGTAAGCCAAAGAAACATTC	571
QY	1032	CTGACGACAGAGCCATTT <td>GAAAGAGCTACAGACCTTGCAAGCAAGAAAGGCTTG</td> <td>1091</td>	GAAAGAGCTACAGACCTTGCAAGCAAGAAAGGCTTG	1091
DB	570	CCAGAGACCAAGAGATCC <td>AGCGTTCCTGCGCGGACAGATTAAGCTCTG</td> <td>511</td>	AGCGTTCCTGCGCGGACAGATTAAGCTCTG	511
QY	1092	TACCAAAAGCAGAAAGAA <td>ATGTACAAAGGATATT</td> <td>1126</td>	ATGTACAAAGGATATT	1126
DB	510	TACCAAAACAGAAAGAG <td>CTGTACAAAGGCTCTT</td> <td>476</td>	CTGTACAAAGGCTCTT	476
RESULT 3				
US-10-425-114-26760				
; Sequence 26760, Application US/10425114				
; Publication No. US2004003488A1				
; GENERAL INFORMATION:				
; APPLICANT: Liu, Jingdong				
; APPLICANT: Zhou, Yihua				
; APPLICANT: Kovalic, David K.				
; APPLICANT: Screen, Steven E				
; APPLICANT: Tabaska, Jack E				
; APPLICANT: Cao, Yongwei				
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With				
; FILE REFERENCE: 38-21(53313)B				
; CURRENT APPLICATION NUMBER: US/10/425,114				
; CURRENT FILING DATE: 2003-04-28				
; NUMBER OF SEQ ID NOS: 73128				
; SEQ ID NO 26760				
; LENGTH: 1432				
; TYPE: DNA				
; ORGANISM: Zea mays				
; FEATURE:				
; OTHER INFORMATION: Clone ID: LIB4574-008-F5_FLI				
US-10-425-114-26760				
Query Match 38.3%; Score 486.8; DB 13; Length 1432;				
Best Local Similarity 71.7%; Pred. No. 6.3e-135;				
Matches 638; Conservative 0; Mismatches 252; Indels 0; Gaps 0;				
QY	237	CCATCTCAAGAGGTAAATGTCCTCCTTAAGTTGATAGAGAACTGAGGCTTGGATGAG	296	
DB	223	CTTCCCAAGAAAGGCGCGCCCAACCCGTTGTTCTCTGACATGAGAGGCCCTTACGAC	292	
QY	297	AAAGTCAGTACAGATTTATTAAGAAAGGTCAAGGTTCCAAACCATCCAAAGTACTCTACA	356	
DB	293	AAAGTTAAGAAAGCAATATCTCAAGAAAGGCCATGCGAAGAAACCGTGAAGTTCCGGAAG	352	
QY	357	TGCTTTTGTCACTACAGGCGCATGACCAAAAATCTCGACACCAATTTGAGATACATGG	416	
DB	353	TGCTTTTGTCACTATGAGCATGCGGTTTCAAGATCATCCGATTAATTTGAGATACCTGG	412	
QY	417	CATGAGCAGCAACCTTATTTGAATTTGTTCTTTGAAAAAGAAAAAAGAACTAGCCGCTTTA	476	
DB	413	CAAGAGCAACATCCATTTGACATGATCTTGGAAAAAGAAAAAACAATGTCCTGTTTA	472	
QY	477	GCCATCGGTTGCTGATGAGAGTCTGGTGAACGAGCGCTTGTCATGTTGGCTGGAA	536	
DB	473	GCCATCGGTTGCTGATGAGAGTCAAGAAAGCGGAGAGCGTGCATTTGTCATGTTGGTGGAG	532	
QY	537	TTAGCTTATGGAAGAAAGAAACCTTTCTTTTCCCAATGTTCCACTATGCGCAGACTTG	596	
DB	533	CTAGCGTATGCAAGAAAGAAAGTTTTCATTTCCCAATGTCCTTCATGCGCAGACTTG	592	
QY	597	TTATATGAGGTGAAGTTATTTGGGTTTATGAAACCAAGAGGAGAAAGCTGCACTGAT	656	
DB	593	GTTTATGAGGTGAAGTTATTTGGATTTGATGATTTGAAGAGGTTAAATCCCGCAAGTGAAC	652	

Qy	ATGACTGTAGAGGAAAAGATTGGTGTGAGACAGACAGAAAGAAAATGATGGGATCTCTT	716
Db	653 ATGACAGTTGAGAGAGAGATTGGACGTGCGACAGACAGAGAAAAGATTGAGGCGAATGCATAT	712
Qy	717 TTTAAGAGAGAAAATCGAGAGAAAGCCATGCAACGATATGAAATGSCCATATGATCAATG	776
Db	713 TTCAAGAAAAGAAAGCTTTGAGAGAGGCCATGCAACATATGAAATGAGGATTCGATACATG	772
Qy	777 GGGAGCATTTTATGTTTTCAGCTGTATGGGAAGTACAGAGTATGGCTTTAGCAGTTAAA	836
Db	773 GGAATATATTTCAATGTTTCAATTATTTTGAGAAAGTACAGAGCATGAGCTTGGCTGTGAA	832
Qy	837 AACCCATGCCATCTTAAACATAGACAGCTTGGCTCATCAACTAAAACGATACGATGAAGCA	896
Db	833 AATCCATGGCATCTCAATATGGCTGCGATGCTGTATCAAACTTAAAGATTCGATGAAGCT	892
Qy	897 ATTGTCATCTGCACATTTGTGTGTGACAGAAAGAGAAAAACCAAAAGCATGTTTCA	956
Db	893 ATTCCGAGGTGACATTTGTTTGTACAGAAAGATTAAGTATATGTCAAAAGCCCTGTTACGG	952
Qy	957 AGAGGAAAAGCAAAAGGACAGAGCTGACAGATGTGACTCAGACCTGTGATTTTCCGAAAG	1016
Db	953 CGAGGAAAAGCTAATATCTGAACCTTGACACAGACGAATTCAGCGAGGAAAGATTTCTCAA	1012
Qy	1017 GCACAAAAGTATGCTCTCTGACGACAAAGCGAATTGAAGAAGCTACGACGACTTGCAGAG	1076
Db	1013 GCGAAGAAGTACTCCACAGAAAGCAAGAGATCATTTGGGAGGCTCCGTTTGCTCGCGGAA	1072
Qy	1077 CAAGAGAAAGCTTGTACCAAAAGCAGAAAGAAATGTACAAAGGAATTT	1126
Db	1073 CAAGACAAGGACTATATCCAGAAAGCAAGAGAGGCTTATCAAAAGGTTCTTT	1122

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RESULT 4
US-10-259-194A-19
; Sequence 19, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghaseemian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Golf, Stephen A.
; APPLICANT: Katagiri, Fumiyuki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Riecke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259, 194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 19
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-194A-19

Query Match          36.5%; Score 463.8; DB 16; length 1082;
Beet Local Similarity 72.0%; Pred. No. 4.3e-128;
Matches 675; Conservative 0; Mismatches 252; Indels 10; Gaps 5;

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OY	129	GAATAGTACTGAAAGGAAGCGCTGTGCAATGTCG-CCATCTCAAGAGGTAACTG	257
Db	34	GAGATACACATGGAAGAACTTCCTTTGTGCACTACGTAGCCCTCTCAAGATGGACCTCTC	93
OY	258	CCTCCTTAAGTTGATAGTGAAGCTGAGGCTCTTGATGGAAGAGTCAGTACAGATTATA	317
Db	94	CAACTGTGTGTTACCTCTGATATGGAAGTCTTATGATTAAGTCAAAAAGCAAGTATCT	153
OY	318	AAGGAAGTCAACGGTTCCAAACCATCGAAGTACTTACATGCTTTTGTCACTACAGGGCA	377
Db	154	AAGGAAGGCATGGCGAAGAAACCCCTCAAGTTTGGCAATGCTTT--GCATATATGAGCA	211
OY	378	TGGAACCAAAACTGCACAGCAAAATTTAGATATACATGCAATGAGCAGACCAACTATTGAA	437
Db	212	TGGGTTCAAGGTTCTTCCGCAAAATTCAGAGATATCTTGCAAGAACACATTCATTTGAA	271
OY	438	TTGGTCTTTGGAAAA--GAGAAAAAAGAATAAGCCGCTTTAGCCATCGGTGTGTACAGAT	496
Db	272	CTAGTACTTGGAAAAAGAAAAAGAAATGACTGTTTAAAGCAATGGTGTCAAGTAAT	331
OY	497	GAAGTCTGTGAACGTGCGCTTGTGCATGTGTGGCAATTTAGCTTATGGAAGAAAGG	556
Db	332	GAGAAGTGGGAGCGTGCATTGTGTCACTGTTAACTGGAGCTGTGCTATGGAAGAAAGG	391
OY	557	AAACTTTCTTTTCCCAATGTTCCACTATGAGCAGACTTTGTTATATGAGGTGAAGTAT	616
Db	392	AAGCTTTTCATTTCCCAATGTCTCTCCATGACACCTTGATATGAAAGTTGAACCTTAT	451
OY	617	TGGGTTTGATGA--AACAAAGAGGAAAAAGCTCGCAGATGATATGACTTAAAGAAAGA	675
Db	452	TGGGTTTATGATGTCAAAAGAGGGGAAAAAGCCGAAGTATATGCAATGGAAGAAAGA	511
OY	676	TTGGTGCACGACAGAAAGAAATGATGGGAATTCCTTTTAAAGAGAGAAACTGG	735
Db	512	TTGAAGCAGCAGACAGAGAAAGATTTGAAGGCAATGAAATATTTCAAGAAAAAGAACTCG	571
OY	736	AGGAAGCATGCAACAGTATGAAATGGCCATATGACATATAGGGGAGCATTTTATGTTTC	795
Db	572	AGGAGGCTATGACGAATATGAAATGGCAATTTGCATATAGGGGATATATTTCAATGTTTC	631
OY	796	AGCTGTATGGGAAGTACCAAGATATGGCTTTAGCAGTTAAAAACCATGCAATCTTAAACA	855
Db	632	AATGTGTTGGGAAGTACAGAGACATGGCTTAGCTGTGAAAAATCCTTGCAATCTCAACA	691
OY	856	TAGCAGCTTGCTCATCAAACTTAAAAAGATACGATGAAGCAATTTGTCATCTCAACA---	912
Db	692	TGGCCGCAATGCTGATCAAACTGAAGAGATTTGATGAAGCTATGCCCCAGTGTACAATY	751
OY	913	--TTGTGTGACAGAAAGAGAAAAACCCAAAAGCACTGTTCAAGAAAGGAAAGCAAA	970
Db	752	GTATGTGTTGTCAGAGATGAAACACAGTGAAMCGTTGTTCAACAGAGAAAAAGCTAG	811
OY	971	GGCAGAGCTAGGACAGATGAGACTGACGACGTGATGATTTCCGAAAGGCAAAAAGTATGC	1038
Db	812	AGCTGAATCTTGTCAAACAGATATGCAAGGAGGACATTTCTGAAAGGCCAAGAAATATTC	871
OY	1031	TCCTGACACAAGGCGATTTAAGAAAGACTTACGACACTTGCAAGCAGAAAGAAAGCCTT	1090
Db	872	TCCAGAAACAAAGAGATTCACGCGGAGCTTCGTCGCTCGGCGAGCAGGATTAAGCTCT	931
OY	1091	GTACCCAAAGCAGAAAGAAATGTACAAAGAAATATTC	1127
Db	932	GTACCCAGAAACAAAAGAGCTATTAACAAAGGCTGTGTTCT	968

RESULT 5
US-10-425-114-29666
; Sequence 29666, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingsong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.

```

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(35313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 29666
LENGTH: 902
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
;
; OTHER INFORMATION: Clone ID: UC-GWFLMINSOY112G04_FLI
US-10-425-114-29666

Query Match      29.3%; Score 372.2; DB 13; Length 902;
Best Local Similarity 72.9%; Pred. No. 1.2e-100;
Matches 499; Conservative 0; Mismatches 178; Indels 6; Gaps 1;

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Qy	531	TGGGAATTAGCTTATGGGAAAGAAAGAAACCTTTCTTTCCCAATGTTCCACTATGGCA	590
Db	1	TGGGAATTAGGATATGGAGAGAAAGAAAGCTTCTCTTTCCAAATGTTCCACCAAGCA	60
Qy	591	GACTTGTTATATGAGGTGAGAACTTATTTGGGTTTGATGAAACAAAGAGCGGAAAGCTGCC	650
Db	61	GATTATGCTTATATGAAAGTTGAGCTTCATGCTGGCTTTGATGAAACCAAGAAAGGCAAGCTGC	120
Qy	651	AGTATATGACTGTAGAGAAAGGATTTGGTGACACAGACAGAAAGAAATATGATGGGAAAT	710
Db	121	AGTATATGACTGTGAGAAAGAAAGGATTTGGTGACAGACACCGAGAAAGATATGATGGAAAT	180
Qy	711	TCTCTTTTAAAGAGGAGAAACTGAGAGAAAGCCATGCAACGATATGAAATGGCCATATGCA	770
Db	181	GCCTTGTATCAGAGAAAGAAACCTGAGAGAGGCTATGCAACAGTATGAAATGGCCATATGCA	240
Qy	771	TACATGGGGGACGATTTTATGTTTCACTGTATGGGAAAGTACAGAGATATGGCTTTAGCA	830
Db	241	TATATGGAGATGACTTCATGTTTCAATGTTTGGAAAGTATAGAGATATGGCTTGGCT	300
Qy	831	GTTAAAAACCCATGCCATCTTAAACATAGCAGCTTGCTCATCAAACTAAAAAGATAGCAT	890
Db	301	GTTAAAGATCATGCTCCATCTTAAACATGGCAGCCTGTTTGATTAAGCTGAACCGCTACGA	360
Qy	891	GAGCAATTGGTCACTGCAACATTGTGTGACAGAAAGAAAGAAACCCAAAGCACTG	950
Db	361	GAACTATAGACATGCAACACTGTACTGGGTGAGATAGGAACAAATGTGAAGGCGTTA	420
Qy	951	TTCAAGAGAGGAAAGCAAGGCGAGACTAGAGACAGATGACATGACAGCTGATGATTC	1010
Db	421	TTTATGGAGAGTAAAGCTTAGAGCAACACTTGGCAAAACAGATGCTGCCAGGGAAGATTTT	480
Qy	1011	CGAAAGCACAAAGTATGCTCCTGACGACAGGCGATTAGAGAGAGCTACGACACTT	1070
Db	481	CTAAAGCCAATTAATATGCCCCCTCAAGACAAAGCAATTTGCTAAAGAAATGAGATTGCTT	540
Qy	1071	GCAGAGCAAGGAAAGCCTGTACCAAAAGCAGAAAGAAATGTACAAAGAAATTTCCAA	1130
Db	541	GCTGAACATGCAAGGCTGTTTACCAAAAGCAGAAAGATATATAAAGGAATATTTGGA	600
Qy	1131	GGGAAAGATGAAGGTGCTGCTAACTCAAAAGCCTTTTTTGGTGTATAGTATTGCA	1190
Db	601	CCAAAGGCTCAACCAAGTTCTTAAGCCAAAGAAAC-----TGGCTCATATCTAATTTGGGAG	654
Qy	1191	TGGTTGGTTCCCTTTTCT	1209
Db	655	TGGTTGCTTTCAGATTTCT	673

RESULT 6
US-10-259-194A-584
; Sequence 584, Application US/10259194A

```
/ Publication No. US20040010815A1
/ GENERAL INFORMATION:
/ APPLICANT: Lange, Markus B.
/ APPLICANT: Ghaseemian, Majid
/ APPLICANT: Briggs, Steven P.
/ APPLICANT: Cooper, Bret
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Goff, Stephen A.
/ APPLICANT: Katagiri, Fumiyaki
/ APPLICANT: Kreps, Joel
/ APPLICANT: Moughamer, Todd
/ APPLICANT: Provart, Nicholas
/ APPLICANT: Rieke, Darrell
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
/ FILE REFERENCE: 70029-NP
/ CURRENT APPLICATION NUMBER: US/10/259,194A
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: US 60/335,277
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/370,743
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/370,620
/ NUMBER OF SEQ ID NOS: 662
/ SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
/ SEQ ID NO 584
/ LENGTH: 864
/ TYPE: DNA
/ ORGANISM: Trilicium aestivum
US-10-259-194A-584
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Query Match      23.5%; Score 298.8; DB 16; Length 864;
Best Local Similarity 73.4%; Pred. No. 1.3e-78;
Matches 395; Conservative 0; Mismatches 142; Indels 1; Gaps 1;

QY 589 CAGACTTGTATATGAGGTGAGAGTTATGGGTTTGTGTAACAAAGAGAGGAAAGCTC 648
DB 1 CAGACCTTATATATGAGTTGAACTCACT-GGTTTGATGCTTAAAGAGGAAAGCTC 59
QY 649 GCAGTATATGACTGTGAGAGAAAGATTGTGCAGACAGACAGAAAGAAATGATGGA 708
DB 60 GTAGTGAATGACGGTATGAGAGAGAGATTGAAACAGCGGATGAGAGAACTTGAGGCA 119
QY 709 ATTCTCTTTTAAAGAGAGAACTGAGAGAACCATGCAACGATGATGAATGCGCATAG 768
DB 120 ACGATTACTTTAAAGAGAAAGAAATTGAGAGGCTATGACAGCAATATGAGATGCGTGTG 179
QY 769 CATACATGGGGAGCGATTTTATGTTTCACTGTATGGGAAGTACAGAGATATGGCTTTAG 828
DB 180 CGTATATGGAGATGATTTATGTTTCACTGTGTTGGGAAGTACAGAGATATGCGCTTTGG 239
QY 829 CAGTAAAAAACCATGCGATCTTAACTATAGCAGCTTCCATCAAACTAAAAAGATACG 888
DB 240 CTGTGAAAAACCGTGCATCTCAACATGCGCTGCTCCATCAAACTAAAAAGATTTG 299
QY 889 ATGAAGCAATTTGCTCACTGCAACATTTGTGTCAGAAAGAGAAAGAAAGCCAAAGCAC 948
DB 300 ACGAACTATCGCAGAGTATGATTTGTCTGTCAAGAGACGAAACCAAGTAAAGCGC 359
QY 949 TGTTCGAAGAGGAGAAAGCAAGCAAGCTAGACAGATGAGACTGACACGATGATTT 1008
DB 360 TGTTCAGACGTGAGAAAGCTAGAGCGAGCTCGGCCAGACAGATTCAGCAGGAGACT 419
QY 1009 TCCGAAGGCAAAAAGTATGCTCTGACAGCAAGCGGATTAAGAGAGCTACGAGCAC 1068
DB 420 TCTTGAAGGCAAGAAACATCTCCCGGAAACAAAGAGATCAAGCGGAGCTTCGGTCCG 479
QY 1069 TTGCAAGCAAGAGAAAGCTTGTATCCAAAGAGAGAAAGAAATGTATCAAAAGATATT 1126
DB 480 TGGCGAAACAAAGATTAAGCATGTACAGAAAGAGAGAGCTATATCAAAAGCTGTGT 537
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RESULT 7
US-09-732-627A-1173
/ Sequence 1173, Application US/09732627A
/ Publication No. US2004012338A1
/ GENERAL INFORMATION:
/ APPLICANT: Fincher, Karen L.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ FILE REFERENCE: 38-21(51770)B
/ CURRENT APPLICATION NUMBER: US/09/732,627A
/ PRIOR FILING DATE: 2000-12-08
/ NUMBER OF SEQ ID NOS: 4930
/ SEQ ID NO 1173
/ LENGTH: 376
/ TYPE: DNA
/ ORGANISM: Gossypium hirsutum
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)-(376)
/ OTHER INFORMATION: unsure at all n locations
/ OTHER INFORMATION: Clone ID: LIB3493-057-Pl-M1-C7
US-09-732-627A-1173
```

```
Query Match      20.0%; Score 254; DB 12; Length 376;
Best Local Similarity 80.4%; Pred. No. 2.2e-65;
Matches 296; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
```

```
QY 462 GAACTAGCCGGTTTACCATCGGTGTTGCTAGCATGAAGCTGTGTAACGTGCGCTTGTG 521
DB 8 GAAATGACTTTTGTGGTATGGTGTGTCAGATGAAATCANAGCAAGTGCATTTGTTA 67
QY 522 CAGTTGGCGTGGAAATTAACCTTATGAGAAAGAAAGAACTTTCTTTCCATGTTCCA 581
DB 68 CAGTGGCGTGGAAATTAAGCTTATGAGAAAGAAAGAAAGCTTTCTTTCCAAAGCTTCA 127
QY 582 CCTATGCGACAGCTTGTATATGAGGTGAGGATTAATGGTTATGGTTATGATGAACAAAGAGAGA 641
DB 128 CCAATGCGACAGATATATATGAGGTGAGCTTATGATTTGATGACAAACAAAGAGAGA 187
QY 642 AAGCTCGCAGTATATGACTGTAGAGAAAGAGATTGTGACAGACAGACAGAAAGAAATG 701
DB 188 AAGGCTCGTGTGACATGACTGTAGAGAAAGAAAGATTGTGACGCGATGAGAAAGATG 247
QY 702 GATGGAATTTCTTTTAAAGAGAGAACTGAGAGAAACCATGCAACATGATGAATG 761
DB 248 GACGGGAATTTCTTTTAAAGAGAGATTAAGCTTAGAGAGAGCCATGCAACATGATGAATG 307
QY 762 GCCATGCAATACATGGGGAGCGATTTTATGTTTCACTGTATGAGGAAAGTACAGATGAG 821
DB 308 GCCATAGCGTACATGGGTATGATCTTTATGTTTCACTGTTATTTGGAAAGATGAGACATG 367
QY 822 GCTTTAGC 829
DB 368 GCTTTAGC 375
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RESULT 8
US-10-259-194A-460/c
/ Sequence 460, Application US/10259194A
/ Publication No. US20040010815A1
/ GENERAL INFORMATION:
/ APPLICANT: Lange, Markus B.
/ APPLICANT: Ghaseemian, Majid
/ APPLICANT: Briggs, Steven P.
/ APPLICANT: Cooper, Bret
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Goff, Stephen A.
/ APPLICANT: Katagiri, Fumiyaki
/ APPLICANT: Kreps, Joel
/ APPLICANT: Moughamer, Todd
/ APPLICANT: Provart, Nicholas
/ APPLICANT: Rieke, Darrell
/ APPLICANT: Zhu, Tong
```

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; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 460
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Musa acuminata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (251)..(251)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (366)..(366)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (437)..(437)
; OTHER INFORMATION: n = any nucleotide
; US-10-259-194A-460

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Query Match      19.8%; Score 252; DB 16; Length 469;
Best Local Similarity 72.1%; Pred. No. 1e-64;
Matches 339; Conservative 0; Mismatches 130; Indels 1; Gaps 1;

QY 237 CCATCTCAGAGGGTAATGTTCTCTCTAAAGTGAATGAAGCTGAGGTTTGATGAG 236
DB 469 CCGGCCAGATGATTAAGATTTACCAAAAGTACGACAGATGAGGTTCTTCATGAG 410

QY 297 AAAGTCATGAAGCATTAATAAGAAAGTCACGGTCCAAACATCCAACTACTAC 356
DB 409 AAAGTCAAAAAGCAAAATTAATAA-GAANGCCATGCTCAAAAACCCAAAAATGTCANT 351

QY 357 TGCCTTTGTCTACAGAGCATGAGCAAAAACCTCGACGCAAAATTTGAGATACATG 416
DB 350 TGCCTTTGTGAATTAATGAGCATGGGTTAAAAAGCATTCACACAAAGTTGAAGATCTGG 291

QY 417 CATGACAGCAACCTATTAATGTTCTTGGAAAAAGAAAAAGAACTAGCCGGTTTA 476
DB 290 CAAGAGCAGCAGCAATTAATTAATTAATGCGAAAAAANAAGCAAGACTGCGTGGTTG 231

QY 477 GCCATCGGTGTGTACATGAAGTCTGTGAAGGTGCGCTTGTGCAATGTTGGTGGGA 536
DB 230 GCATTCGGCATGTCTACATGAAGAGTGGGAAAGTGCACCTCTTCAATGCGGTGGGA 171

QY 537 TTAGCTATGAGGAAAGAAAGAACTTTTCTTTCCATGTTCCACCTATGGCAGACTTG 596
DB 170 CTGGCTACGGGAAAGAAAGAAATTTTTCATTTCCCAAAAGTCCCCCTTAAGCAGACTT 111

QY 597 TTATATGAGGTGAAGTATGTTGGTTGATGAACAAAGAGGAAAAAGCTCGCAGTAT 656
DB 110 GTTATATGAGGTGAAGTATGTTGGTTGATGAAGCCAAAGAGGAAAAAGCCCGAGTGAC 51

QY 657 ATGACTTAAGAGAAAGATTTGTGACGACGACAGCAAGAAATGATG 705
DB 50 ATGACGTAGAAGAGAGATTGAAGCTGCGCAAAAAGAAAGGATGGAAG 2

```

```

RESULT 9
US-10-424-599-138708
; Sequence 138708, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 138708
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1458)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96260C.1
; US-10-424-599-138708

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Query Match      16.6%; Score 210.4; DB 13; Length 1458;
Best Local Similarity 68.3%; Pred. No. 6.6e-52;
Matches 362; Conservative 0; Mismatches 91; Indels 77; Gaps 2;

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QY 455 GAAAAAAGACTAGCCGGTTTGTAGCCATCGGTGTGTACATGAATGAATGCTGTAACGTCG 514
DB 36 GAGGAAAGAAATGACTGCGGTGGGCAATGGTGTGGCAAGCATTAAGCTGGGAGCGTCG 95

QY 515 GCTTGTGATGTTGGCTGGGAATTAAGCTTAAGGAAAGAAAGAACTTTTCCCA 574
DB 96 GTTGTGCGGTGTGGCTGGGAATTAAGATATGAGAGAAAGAAAGCTTCTTTTCCAA 155

QY 575 TGTTCACCTATGCGACACTGTTTATATAGAGTGAAGTATTTGGGTTGATGAACAA 634
DB 156 TGTTCACCCCAAGCAGATTTAGTTATGAAGTTGACTATGGCTTTGATGAACAA 215

QY 635 GG----- 636
DB 216 AGAAGTAATGGCATTAAATTAATGATGCGTGTGACCTTGTAGATGCTTATAGCACC 275

QY 637 -----AGGAAAAGCTCGCAGTGAATGAATGAGAAAGAAAGATTGTGACAG 687
DB 276 TGATTTACAGGGGAAAGCTCGCAGTGAATGATGCTGTGAGGAAAGAAATTTGGTGCAG 335

QY 688 ACAGAAAGAAATGATGGAATTTCTTTTAAAGAGAAAGAACTGAGAGAACCATGC 747
DB 336 ACCGAGAGAAAGATGAGTGAAGAACTTTGTATCAGAAAGAAAGAACTGAGAGAGCTATGC 395

QY 748 AACAGTATGAATAGGCATATGATGATGAGGAGAGCAATTTTAAAGTTTACGCTATGAGGA 807
DB 396 AACA-----GCCATTGCAATATGAGGAGATGATCTTCATGTTCCAGTTGTGGGA 445

QY 808 AGTACAGATATGAGCTTTTATGAGCTTAATAAAACCATGCCATCTTAACATAGCAGCTTGC 867
DB 446 AGTATGAGATATGAGCTGTGCGAGTAAAGATCAATGCCATCTTAACATAGGAGCGCTGT 505

QY 868 TCATCAAACTAAAGATACATGATGAAGCAATTTGTGCTACGCAACATTTG 917
DB 506 TGATTAAGCTGAACCGCTACGAAGAGCAATGAGCAATGCAAGCAATTTG 555

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RESULT 10
US-10-437-963-88914
; Sequence 88914, Application US/10437963

```

```
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovacic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barabuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 88914
/ LENGTH: 602
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_8771C.1
US-10-437-963-88914

Query Match          16.1%; Score 204.4; DB 17; Length 602;
Best Local Similarity 65.6%; Pred. No. 2.4e-50;
Matches 298; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 199 GAATACTTACTGAGAGAGTGCCTGTTGTCATAGTGGCCATCTCAAGAGGTAATGTC 258
DB 149 GAGATATACGAGGAGATTAATCTCTGTGTGCACATGAACCTCTTGATGGGCTGTCTC 208
QY 259 CTCTTAAGTTGATAGTGAAGCTGAGGTCTTTGATGAGAAATGCAATGACATTTTAA 318
DB 209 CACCTGTGCTTACCTGTGATATGAGAGCCCTTAATGAAAGCCAGAAACCAAGGCATCA 268
QY 319 AGGAAGTGCAGCGTTCCAAACATCCAAAGTACTCTACATGCTTTTGTCACTACAGGCGAT 378
DB 269 AGAATATCCATGCGCAAGAAACCTCTCAAGTTTGACACATGCTTTGTTCACTATACAAAT 328
QY 379 GGAACAAAACCTGCGACACAAATTTGAGATACATGAGCATGAGCAGCAACCTAATGAT 438
DB 329 GGGTTCAGAGTTCTTGCAAAATTCGAGATACCTTGGAAGAACACATTTGATGAC 388
QY 439 TGGTCTTGAGAAAGAGAAAGAAAGAAATAGACCGGTTTACCATCGTGTGCTAGCATGA 488
DB 389 TAGTACTTGGAAAAACAGAAAAAGAACTGACTGTCTMAAGCTTGTGCGCCACTAATGTA 448
QY 499 AGTCTGTGAACGTGCGCTGTGTGATGTGGCTGGGAATTAGCTTATGGAGAAAGAA 558
DB 449 AAAGAGGGAGCGCTGCTTTGTTACATGTGTAATGCGAGCTTGCTATGTTAAACAGAA 508
QY 559 ACTTTTCTTTTCCCAATGTTCACCTATGCGAGACTTGTATATGAGGTGAAGTTATG 618
DB 509 GCTTTTATATCCCAATAGTTCTCTCAATGCGAGCCCTGTATATGAAGTGAATCTACTG 568
QY 619 GGTTCATGAACAAAGAGAGAGAAAGCTGCGAG 652
DB 569 GGCCTTGTATGTCTACAGAGAGAAAGCCCGAAG 602

RESULT 11
US-09-770-445-291
/ Sequence 291, Application US/09770445
/ Patent No. US20020023281A1
/ GENERAL INFORMATION:
/ APPLICANT: Gorlach, Jorn
/ APPLICANT: An, Yong-Qiang
/ APPLICANT: Hamilton, Carol M.
/ APPLICANT: Price, Jennifer L.
/ APPLICANT: Raines, Tracy M.
/ APPLICANT: Yu, Yang
/ APPLICANT: Rameaka, Joshua G.
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/ APPLICANT: Page, Amy
/ APPLICANT: Matthew, Abraham V.
/ APPLICANT: Bedford, Brooke L.
/ APPLICANT: Moessner, Jeffrey P.
/ APPLICANT: Haas, William David
/ APPLICANT: Garcia, Carlos A.
/ APPLICANT: Kicker, Maja
/ APPLICANT: Slader, Ted
/ APPLICANT: Davis, Keith R.
/ APPLICANT: Allen, Keith
/ APPLICANT: Hoffman, Neil
/ APPLICANT: Hurban, Patrick
/ TITLE OF INVENTION: Expressed Sequences of Arabidopsis
/ TITLE OF INVENTION: thaliana
/ FILE REFERENCE: 2023US (PARA-012PRV)
/ CURRENT APPLICATION NUMBER: US/09/770,445
/ CURRENT FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: US 60/178,472
/ PRIOR FILING DATE: 2000-01-27
/ NUMBER OF SEQ ID NOS: 999
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 291
/ LENGTH: 968
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-770-445-291
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Query Match          10.0%; Score 126.6; DB 9; Length 968;
Best Local Similarity 77.7%; Pred. No. 7.6e-27;
Matches 178; Conservative 0; Mismatches 49; Indels 2; Gaps 2;

QY 436 AATTGTTCTTGAAGAAAGAAAGAAAGAACTAGCCGCTTACCATCGGTGTTGCTAGCA 495
DB 68 AATGCTCTATGAAGAGATACAGATATGAGCCGCTTATGCTATGTTGTTTCCAGCA 127
QY 496 TGAAGTCTGTGAACGTGCGCTTGTGCATGTTGCTGGAA--TTAGCTTATGGAGAA 554
DB 128 TCAAGTCTGTGAACGTGCGCTTGTGCATGTTGCTGGAAATTACATATAGAGAGAT 187
QY 555 GGAACCTTTTC--TTTCCCAATGTTCCACCTATGCGAGACTTGTATATGAGGTGAAGT 613
DB 188 GGAACCTTTCTTTTCCCAATGTTCCATCTATAGCGGAATGTTAGATGACGCTGAAGT 247
QY 614 TATTGCTTGTATGAACAAAGAGAGAAAGTCCCATGATATGACT 662
DB 248 GTTGTATGTATGAACAAAGAGAGAACGTTTTCCTTAAGATCATT 296
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RESULT 12
US-10-425-114-34960
/ Sequence 34960, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E.
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 34960
/ LENGTH: 1171
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: UC-ZMFLMO17365D08_F11
US-10-425-114-34960
```

Query Match 8.2%; Score 103.6; DB 13; Length 1171;
 Best Local Similarity 48.8%; Pred. No. 6,9e-20;
 Matches 410; Conservative 0; Mismatches 409; Indels 21; Gaps 4;

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QY      291 GATGAGAAAGTCAGTAAAGCAAGATTATTAAGAAAGTCAAGGTTCCAAACATCCAAAGTAC 350
      44 GATAGAGAAATCCCTTAAGAAAGTCTCAAGAGAGGAAAGATTATGAGCGTCCCAACGAG 103
QY      351 TCTACATGCTTTTGCTACCTACAGGGCATGAGCCAAAACCTCGACGCAAAATTGAGAT 410
      104 GGTGCTGTGTGTGAAGTCAAAATTAATCGGAAAGCTTCAGATGCGCGGTGTACAAAG 163
QY      411 ACATGCGATGAGCAGCAACCTATTGAATTGGTTCTTGAAAGAGAAAAAGAACTAGACC 470
      164 AAGGGGATGACGAAAGAGCCATTTAATTCAGAGCCGATGAAGG---GAAATTATTGCC 220
QY      471 GGTTAAGCCATCGGTGTGCTAGCATGAAGTCTGCTGAAAGCGTGCGCTTGTCATGTTGGC 530
      221 GGTCTTGATCGTGTGTGTGAACATGAAAGAGGCGAGGTGCTCTGTGCACAAATTCCT 280
QY      531 TGGGAATTAGCTTATGGG---AAAGAGGAAACCTTTCTTTCCCAATGTTCCACCTATG 587
      281 CTTGAATATGCAATTTGTTCAACTGAGTCAAGAGAGGATCTTGCTGTGTTCCACTTAC 340
QY      588 GCAGACTTGTATATAGAGTGAAGTATGTTGGTTTGATGAAACAAAGAGGAGAAAGCT 647
      341 AGCAGATATATATAGAAAGTTGAGCTTATTCAATTTTGAAAGCAAGAGTGTG----- 395
QY      648 CGCAGTATATGACTGTAGAGAAAGATTGGTGCAGACAGACAGAAATAATGATGGG 707
      396 ---GGGACTTGAACAAAGAGAAAGATGAGGCTGCTGTGAAGAAAGAGGAGG 451
QY      708 AATTCCTTTTAAAGAGGAGAAACCTGAGAGAGCCATGACATGATGTAATGGCCATA 767
      452 AATGCAATTGTTCAATCGGCAAAATATGCTAGAGCTTCCAGGATATGAGAGGCTGCC 511
QY      768 GCATACATGAGGAGCAATTTATGTTTCACTGTATGGAAGTACACAGATATGCTTTA 827
      512 AAGTACATGATGATGACGACCTTGCTTCAAGTATGAGAAAGCAATCCAG----- 565
QY      828 GCACTTAAAAACCATGCTTAAATATAGAGAGCTTGCCTCATCAAACTAAAAAGTAC 887
      566 CAACTGAAGATCAGCTGCAACTTAACAAATGCTGCCGCAACGAAAGTGAAGGATTAC 625
QY      888 GATGAAGCAATGGTCTCACTGCAACATGTTGTGACAGAGAAAGAGAAACCCAAAAGCA 947
      626 AAGGAGCTCGAAGCTTTGCAACCAAGTTCTGGAATAGACACCCAAAATGTCAGAGCT 685
QY      948 CTGTTCAAGAGGAGGAGAAAGCAAGAGCTAGAGACATGATGATGATGATGATGAT 1007
      686 CTCTACAGAGAGGAGGAGGCTTACATTCATCACTTGCTGACCTAGAGCTAGAGGCGGAT 745
QY      1008 TTCCGAAAGGACAAAAGTATGCTCTCTGACGACAGAGCGCATTAAGAGAGCTACAGCA 1067
      746 ATCAAAAAGGACATGAAATGATCTTGACAAACAGGAGATGTCAGATTATTAAGATC 805
QY      1068 CTTGACAGAGAGAGAGAGCTTGTATCAAAAGAGAGAAAGAAATGTCAGAAAGATTTTC 1127
      806 CTGAAGAGAGAGATCAAGAGATACACAAAGAGAGCCCAAAATTTCTACAGCAATGTTCC 865
  
```

RESULT 13

US-10-310-154-128

; Sequence 128, Application US/10310154

; Publication No. US20030233670A1

; GENERAL INFORMATION:

; APPLICANT: Edgeton, Michael D

; APPLICANT: Chomet, Paul S.

; APPLICANT: Adams, Thomas H

; APPLICANT: Ruff, Thomas G.

; APPLICANT: Agarwal, Ameeta K.

; APPLICANT: Antens, Jeffrey E.

; APPLICANT: Ball, James A.

```

; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Kolian
; APPLICANT: Dong, Jinhua
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jindong
; APPLICANT: Lu, Bin
; APPLICANT: Luehy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, ManchiKanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Temmesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 128
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(1757)
; OTHER INFORMATION:
  
```

US-10-310-154-128

Query Match

8.2%; Score 103.6; DB 16; Length 2019;

Best Local Similarity 48.8%; Pred. No. 9.8e-20;

Matches 410; Conservative 0; Mismatches 409; Indels 21; Gaps 4;

```

QY      291 GATGAGAAAGTCAGTAAAGCAAGATTATTAAGAAAGTCAAGGTTCCAAACATCCAAAGTAC 350
      921 GATAGAGAAATCCCTTAAGAAAGTCTCAAGAGAGGAGAAAGTATGAGCGTCCCAACGAG 980
QY      351 TCTACATGCTTTTGCTACCTACAGGGCATGAGCCAAAACCTCGACGCAAAATTGAGAT 410
      981 GGTGCTGTGTGTGAAGTCAAAATTAATCGGAAAGCTTCAGGATGCGCGGTGTACAAAG 1040
QY      411 ACATGCGATGAGCAGCAACCTATTGAATTGGTTCTTGAAAGAGAAAAAGAACTAGACC 470
      1041 AAGGGGATGACGAAAGAGCCATTTAATTCAGAGCCGATGAAGG---GAAATTATTGCC 1097
QY      471 GGTTAAGCCATCGGTGTGCTAGCATGAAGTCTGCTGAAAGCGTGCTTGTCATGTTGGC 530
  
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Db 1098 GGTCTTGATCGTCTGTGTGAACATGAAAGAGGCGAGTTGCTTGTCACAATTCCT 1157
Qy 531 TGGGAATTAGCTTATGGG---AAAGAAGAAACCTTTCTTTTCCCAATGTTCCACCTATG 587
Db 1158 CCGTAATATGCTATTTGGTCACTGAGTCAAGAGGATCTTGTGTTTCCACCTTAC 1217
Qy 588 GCAGACTTGTATATAGTGAAGTATATGAGTTGAGTTGATGAAACAAAGAGGAGAAAGCT 647
Db 1218 AGCAGCTATATATATGAGTGAAGTATATTCATTTTGTGAAGACAGAGAGTGTGCT----- 1272
Qy 648 CGCAGTATATGACTGTAGAGAAAGGATTTGTGACAGACAGAAAGAAATGATGGG 707
Db 1273 ----GGGACTTGAACATGAAGAGAGATTTAGGCTCTGTATGAAGAAAGAGAGGG 1328
Qy 708 AATTTCTTTTAAAGAGAGAAACCTGAGAGAACCTGCAACATGTGAATGAGCCATA 767
Db 1329 AATGCAATTTGTCAAATGGGCAATATATCTAGAGCTTCCAAAGCATATGAGAGGCTGCC 1388
Qy 768 GCATACATGGGGGACGATTTTATGTTTCACTGTATGGAAGTACAGAGATATGGCTTTA 827
Db 1389 AAGTACATTTAGTATGACACTTGTCTGATGAGATGAGAAAGCAATCCAG----- 1442
Qy 828 GCAGTTAAAAACCATGCTCACTTAACTAGACAGCTTGCCTCACTCAAACTAAAAAGATAC 887
Db 1443 CAATGAAAGATCAAGCTGCAACCTAAACATGCTGCTGCAAACTGAAATGAAAGATTAC 1502
Qy 888 GATGAAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAACCCAAAAGCA 947
Db 1503 AAGGAAGCTCGAAGCTTTTGCACACAGTTCTGACATGACAGCCAAAATGTCAAGGCT 1562
Qy 948 CTGTTCAAGAGAGAGAAAGCAAGGACAGCTAGAGACAGATGAGCTCAGACAGCTGATAT 1007
Db 1563 CTCTACAGAGAGGCTGCAAGCTTACATTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1622
Qy 1008 TTCCGAAGGACAAAAGTATGCTCTGACAGACAGGCGATTTAGAAAGAGCTTACAGCA 1067
Db 1623 ATCAAAAAGGCACTGAAATTCGATCTGACACAGGAGATGCAAGTTGAATTAAGATC 1682
Qy 1068 CTTCAGAGACAAAGAAAGCTTGTATCCAAAGCAAGAAAGAAATGTACAAAGAAATTTTC 1127
Db 1683 CTGAAGAGAAAGATCAAGAGATGCAACAGAAAGACCCAAATTTCTACAGCAACATGTTCT 1742

RESULT 14
US-10-425-114-13768
; Sequence 13768, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack B.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 13768
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-040-E3_FLI
US-10-425-114-13768
Query Match 8.1%; Score 102.8; DB 13; Length 1617;
Best Local Similarity 50.9%; Pred. No. 1,5e-19;
Matches 329; Conservative 0; Mismatches 302; Indels 15; Gaps 3;
Qy 402 TTGAGGATCATGCGATGACGACGACATTAATGATGTTGTTGGAAAAAGAAAAAA 461
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Db 608 TTTGTAAGAAAGGCGATATGATGTAAGAGCCTTTGAATTAAGACAGATGAGGACG 667
Qy 462 GAACATGCGGCTTTAGCCATCGGTGCTGACATGAAGTCTGTGAAGCTGGCTTGG 521
Db 668 GTTATGAAAGGCGCTTCAATTAACGATGATTAATATGAAGAAAGAGAGTGGTGGCT 727
Qy 522 CATGTGGCGGGAATTAAGTATGAG---GAAAGAAAGAAACCTTTCTTTCCCAATGTT 578
Db 728 AGAGTACCACTGAAACAGATTTGATGCTGTAGAAACAAATCAAGATCTTGCTACTGTT 787
Qy 579 CCACTATGAGCAGACTTGTATATATGAGTGAAGTATGAGTTGAGTTGATGAAACAAAGAG 638
Db 788 CTTCTAATTTTACCGCTTTGTATGAGTGAAGTGGAGCTGTTTCTTTAG-----AAGAG 841
Qy 639 GGAAGAGCTGCGAGTATATGACTGTAGAGAAAGATTTGTGACAGACAGAGAAAA 698
Db 842 AAGAAATCTTGGGACTTGAAGACCAATATTGAGAAATGAAAGCAGCTGCCAAGAGAAA 901
Qy 699 ATGATGAGGAATTTCTTTTAAAGAGAGAAACCTGAGAGGACATGACATATGAA 758
Db 902 GATGAAGGAAATGTGTTTCAAGATGGGCAAGTACCAAGGCTCCAAAGATACGAG 961
Qy 759 ATGCCATAGCATACATGAGGAGGACGATTTTATGTTTCACTGTATGGAATACAGAT 818
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Qy 819 ATGCTTTAGAGCTTAAAAACCATGCACTTAACTAGACAGCTTCTCAATCAACTA 878
Db 1022 AAGCTCTG-----AAGTCAAGTTCCAAGCTCAAGTCAAGAGCCCTGCAAGCTGAAGT 1075
Qy 879 AAGCATAGATGACAAATTTGCTCCTGCAACATTTGTGTACAGAAAGAGAAAG 938
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Qy 939 CCAAAAGCACTGTTCAAGAGGAGAAAGCAAGGACAGCTAGAGACAGATGACCTGCA 998
Db 1136 GTTAAAGCCTTTGACAGAAAGGAGGAGCATATGAGCTTTGTTGCTAGAGCTAGCA 1195
Qy 999 CGTATGATTTTCCGAAGGACAAAAGTATGCTCTGACAGACAGG 1044
Db 1196 GAGTTGATGTGTAAGAAAGCACTGAAATTTGATCTGATTAACAGG 1241

RESULT 15
US-10-424-599-31694
; Sequence 31694, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 31694
; LENGTH: 2568
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) - (2568)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_128624C.1
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Query Match 7.6%; Score 96.6; DB 13; Length 2568;
Best Local Similarity 49.4%; Pred. No. 1.4e-17;
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Matches 348; Conservative 0; Mismatches 339; Indels 18; Gaps 3;

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Db 1183 AGATGAGAAACAAGTGTATGATGACTTGAATAGACTGTATGATGATGAGAAAGGTGA 1242
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QY 509 ACGTGCCTTGTGCATGTGCTGGGAATTAAGTTATG--GAAAGAGAAACTTTTC 565
    |||||
Db 1243 GGTTCACCTGTGACCATGCACTGCAATATGCTTTTGTTCATCAGATCCAGCAGGA 1302
    |||||
QY 566 TTTTCCCAATGTTCCACTATGCGACACTGTTATATAGAGTGAAGTATTTGGTTTGA 625
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Db 1363 GAAAGAGAGAGAG-----TCTTGGATTTGAACACTGAAAGAGAACTGAAAGCTGC 1413
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QY 686 AGACAGAGAAAAATGATGAGAAATCTCTTTTAAAGAGAGAAACTGAGAGAAAGCCAT 745
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Db 1414 TGGTAAGAGAGAAAGAGAAAGATGTGTGTTTAAAGCTGTAGCATGCAAGAGCTTC 1473
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QY 746 GCAACAGTATGAATGGCCATAGCAATACATGGGGACGATTTATGTTTCACTGTATGG 805
    |||||
Db 1474 CAAAAGATATGAAAGGCTGTAAAGTACATAGATATGATTCCTCATTCGTTGAGAGGA 1533
    |||||
QY 806 GAAGTACAGAGATATGCTTTAGCAATTAAGAAACCCATGCCATGCTTAACATAGCAGCTG 865
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Db 1534 GAAAAAGCAGGCCAAGACCTTGAAGTT-----GCTGCAATCTTAACAATGCTGCTTG 1587
    |||||
QY 866 CCTCATCAAACTAATCAATACGATGAGCAATTTGTCACCTGCAACATTTGTGACAGA 925
    |||||
Db 1588 CAAGTTGAAGTTAAAGACTACAGAGAGAGAAATTTGTATCAAGGTGTTAGACT 1647
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QY 926 AGAAGAGAAAAACCAAAAGCACTGTTCAAGAGAGGAAAGCAAGGCAAGCTAGGACA 985
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Db 1648 CGAGAGTACAAATGTTAAAGCCCTCTATAGAGGGCCCAAGCATATATGCAAGTTACTGA 1707
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QY 986 GATGACTCAAGCAGTATGATTTCCGAAAGGCACAAAAGTATGCTCTGACGACAGGC 1045
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Search completed: July 7, 2004, 22:27:51
Job time : 833 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 16:21:19 ; Search time 5090 Seconds

(without alignments)
7450.878 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270
Sequence: 1 gaagaagtcgaagggctctc.....atgaagaaggggtacacatca 1270

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_estin: *
3: em_estin: *
4: em_estin: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_estc: *
9: gb_est1: *
10: gb_est2: *
11: gb_est3: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrc: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rnd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	693.2	54.6	741	13	BU635657 028D02 In
2	673.4	59.4	9	AV784851	AV784851 AV784851
3	649	51.1	669	9	AV823798 AV823798
4	608.4	47.9	650	14	CB255740 CB255740 23-E01274

5	490	38.6	892	14	CB981020
6	464.4	36.6	1363	11	AY105475
7	449.6	35.4	972	14	CP436078
8	429	33.8	710	14	CP417393
9	395.6	31.1	839	14	CA765208
10	391.6	30.8	650	10	AW773636
11	380.2	29.9	812	14	CB659598
12	374.8	29.5	705	13	BU67926
13	354.4	27.9	699	13	BO994520
14	341.4	26.9	667	12	BG451848
15	333.4	26.3	493	14	CP23456
16	330.8	26.0	583	10	BE455629
17	326.6	25.7	674	12	BM110915
18	322.8	25.4	471	10	BE209658
19	320.4	25.2	710	12	B566970
20	319	25.1	532	13	BUS77634
21	317.2	25.0	531	13	BO987397
22	312.8	24.5	758	14	CA196409
23	310.6	24.6	813	14	CP430474
24	291.6	23.0	637	9	AV916516
25	290.6	22.9	845	14	CB659599
26	286.4	22.6	772	14	CP430421
27	283	22.3	358	29	BA97643
28	281.6	22.2	699	14	CD894285
29	279	22.0	661	14	CA185500
30	276.4	21.8	806	14	CB683163
31	274	21.6	469	10	AW222544
32	271.8	21.4	380	29	BA97644
33	264.4	20.8	538	13	BU878153
34	258.2	20.3	645	10	BF646472
35	255.6	20.1	812	28	BH557130
36	252.6	19.9	483	9	AU225473
37	248	19.5	479	10	AW428872
38	247	19.4	490	12	BG462802
39	246	19.4	705	14	CD207807
40	243.6	19.2	655	14	CD883248
41	240.6	18.9	557	10	AW441601
42	240.6	18.9	648	13	CA120169
43	239.2	18.8	445	12	BG553433
44	237.2	18.7	636	9	AV925548
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ALIGNMENTS

RESULT 1
BU635657 741 bp mRNA linear EST 23-SEP-2002
DEFINITION 028D02 Infected Arabidopsis Leaf Arabidopsis thaliana CDNA, mRNA

LOCUS
BU635657
ACCESSION
BU635657
VERSION
BU635657.1 GI.23302912
KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1 (bases 1 to 741)
Lundgaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.

AUTHORS
and Weindler, K.G.
EST sequencing of Erysiphe cichoracearum infected Arabidopsis
plants

TITLE
Unpublished (2002)
COMMENT
Contact: Karen G. Weindler
Institute for biotechnology
Aalborg University
Solngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk.
Location/Qualifiers

FEATURES

source

1. .741
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia"
/db_xref="taxon:3702"
/dev_stage="Plant 3 weeks old, three days post infection"
/clone_lib="Infected Arabidopsis leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. choroacearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dt selected."

ORIGIN

Query Match 54.6%; Score 693.2; DB 13; Length 741;
Best Local Similarity 99.4%; Pred. No. 1.2e-164;
Matches 732; Conservative 0; Mismatches 8; Indels 4; Gaps 3;

222 CGTTGTCATAGTGGCCATCTCAAGAGGGTAATGTTCTCTTAAAGTTGATGTAAGCT 281
1 CGTTGTCATAGTGGCCATCTCAAGAGGGTAATGTTCTCTTAAAGTTGATGTAAGCT 58
282 GAGGCTTTGATGAGAAAGTCAGTAAGCAATTATTAAGAGAGTCAAGCTTCCAAACCA 341
59 GAGGCTTGGAGTGAAGAGTCAGTAAGCAATTATTAAGAGAGTCAAGCTTCCAAACCA 118
342 TCCAGAGTCTTACATGCTTTTGTCACTACAGGCGCATGACCAAAAAGTCCAGACAA 401
119 TCCAGAGTCTTACATGCTTTTGTCACTACAGGCGCATGACCAAAAAGTCCAGACAA 178
402 TTGAGAGATCATGCGATGAGCAGCAACCTATTAATGTTGTTTGGAAAAAGAAAAA 461
179 TTGAGAGATCATGCGATGAGCAGCAACCTATTAATGTTGTTTGGAAAAAGAAAAA 238
462 GAATGACCGGTTTATGCAATGCTGTTGCTGATGAAAGTCTGTAAGTCTGCTTGTG 521
239 GAATGACCGGTTTATGCAATGCTGTTGCTGATGAAAGTCTGTAAGTCTGCTTGTG 298
522 CATGTTGGCTGGGAATGAGCTTATGGAAGAAAGAAATTTTCTTTCCCAATGTTCCA 581
299 CATGTTGGCTGGGAATGAGCTTATGGAAGAAAGAAATTTTCTTTCCCAATGTTCCA 358
582 CCTATGCGAGCTTGTATATGAGTGAAGTTATGAGTTTGAATGAACCAAGAGGGA 641
359 CCTATGCGAGCTTGTATATGAGTGAAGTTATGAGTTTGAATGAACCAAGAGGGA 418
642 AAAGCTGCGATGATGATGATGAGAGAAAGATTGGTGAAGAGAGAGAGAGAGAGAG 701
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702 GATGGAATTCCTTTTAAAGAGAGAGAACTGAGAGAGCATGCAACAGTATGAATG 761
479 GATGGAATTCCTTTTAAAGAGAGAGAACTGAGAGAGCATGCAACAGTATGAATG 538
762 GCCATAGCATATGAGGAGAGCATTTTATGTTTCACTGATGAGAAAGTACAGATATG 821
539 GCCATAGCATATGAGGAGAGCATTTTATGTTTCACTGATGAGAAAGTACAGATATG 598
822 GCTTTAGCAGTTAAAAAACCATGCACTTTAATACATAGCAGTTCCCTCATC-AAACTAAA 880
599 GCTTTAGCAGTTAAAAAACCATGCACTTTAATACATAGCAGTTCCCTCATC-AAACTAAA 658
881 ACGATAGAGTAAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAAACC 940
659 ACGATAGAGTAAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAAACC 717
941 AAAAGCACTGTTCAAGAGAGGAA 964
718 AAAAGCACTGTTCAAGAGAGGAA 741

LOCUS AV784851 694 bp mRNA linear EST 28-MAR-2002
DEFINITION AV784851 RAFL6 Arabidopsis thaliana cDNA clone RAFL06-08-N18 3',
mRNA sequence.
ACCESSION AV784851
VERSION AV784851.1 GI:19803641
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 694)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SctI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for
further details.

FEATURES

Location/Qualifiers

1. .694
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL06-08-N18"
/dev_stage="Plants at various developmental stages from
germination to mature seeds"
/lab_host="DH10B"
/note="Site 1: SctI; Site 2: XhoI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"

ORIGIN

Query Match 53.0%; Score 673.4; DB 9; Length 694;
Best Local Similarity 99.7%; Pred. No. 1.2e-159;
Matches 685; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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694 TATGCGAGCTTGTATATGAGTGAAGTTATGAGTTTGAATGAACCAAGAGGAAA 635
644 AGCTCGAGTATATGATGATGAGAGAAAGATTGGTGAAGAGAGAGAGAGAGAGAG 703
634 AGCTCGAGTATATGATGATGAGAGAAAGATTGGTGAAGAGAGAGAGAGAGAGAG 575
704 TGGGAATTCCTTTTAAAGAGAGAACTGAGAGAGCATGCAACAGTATGAATGAG 763
574 TGGGAATTCCTTTTAAAGAGAGAACTGAGAGAGCATGCAACAGTATGAATGAG 515
764 CATAGCATATGAGGAGAGCATTTTATGTTTCACTGATGAGAAAGTACAGATATGAG 823
514 CATAGCATATGAGGAGAGCATTTTATGTTTCACTGATGAGAAAGTACAGATATGAG 455
824 TTTAGCAGTTAAAAAACCATGCACTTTAATACATAGCAGTTCCCTCATCAACTAAAAG 883
454 TTTAGCAGTTAAAAAACCATGCACTTTAATACATAGCAGTTCCCTCATCAACTAAAAG 395
884 ATAGAGTAAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAAACC 943
394 ATAGAGTAAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAAACC 335

QY 944 AGCACTGTTCCGAAAGAGGAAAGCAAGAGCAGACTAGACATGAGTCAAGCAGCTGA 1003
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DB 334 AGCACTTTCAGAAAGAGGAAAGCAAGAGCAGACTAGACATGAGTCAAGCAGCTGA 275
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QY 1004 TGAATTTCCGAAAGGACAAAAGTATGCTCTGACGACAAAGCGATTGAAAGAGCTACG 1063
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DB 274 TGAATTTCCGAAAGGACAAAAGTATGCTCTGACGACAAAGCGATTGAAAGAGCTACG 215
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QY 1064 AGCACTGTCAGAGCAAGAAAGGCTTGTATCCAAAGACGAAAGAAATGTATCAAGAAAT 1123
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DB 214 AGCACTTTCAGAGCAAGAAAGGCTTGTATCCAAAGACGAAAGAAATGTATCAAGAAAT 155
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QY 1124 ATTCAAGAGGAAAGATGAAGGTGTGCTTAA-GTCAAGAGGCTTTTGTGTAGTAGTGT 1182
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DB 154 ATTCAAGAGGAAAGATGAAGGTGTGCTTAAAGAGGCTTTTGTGTAGTAGTGT 95
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DB 94 TATGCAATGTTGTTTCCCTTTTCTCCGATCTTTTGAAGCCGACAGATTAAAGCAG 35
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DB 34 ATTATATGATGAAGAGGTTACAAT 8
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AV823798 669 bp mRNA linear EST 01-APR-2002
LOCUS AV823798 RAF16 Arabidopsis thaliana cDNA clone RAF16-08-N18 5',
DEFINITION mRNA sequence.
VERSION AV823798
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Arabidopsis thaliana
AUTHORS Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 669)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SefI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for
further details.
FEATURES
Location/Qualifiers
1..669
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAF16-08-N18"
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hr) treatments"

ORIGIN

Query Match 51.1%; Score 649; DB 9; Length 669;

Best Local Similarity 99.1%; Pred. No. 1,8e-153;
Matches 663; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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DB 1 TGAAGATCAAAATTCGAAATTTATCTCTGCTGATGATCAGTCTTGTGATGATCTTCGAC 60
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QY 88 GACGAGAGAGTCACTACTCTTGAAGCTTCTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 147
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DB 61 GACGAGAGAGTCACTACTCTTGAAGCTTCTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 120
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QY 148 ATATGATGATGATCTCTGAGATCACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAA 207
| | | | |
DB 121 ATATGATGATGATCTCTGAGATCACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAA 180
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QY 208 ACTGAAGAAAGTCCGCTTGTGATGATG-CCCATCTCAAGAGGTTATGTTCTCTTAA 266
| | | | |
DB 181 ACTGAAGAAAGTCCGCTTGTGATGATG-CCCATCTCAAGAGGTTATGTTCTCTTAA 240
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QY 267 GTTGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 326
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DB 421 GGAAG 480
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DB 481 GAACGTGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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QY 567 TTTCCGATGTTCCACCTTATGAG 626
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DB 541 TTTCCGATGTTCCACCTTATGAG 600
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QY 627 GAAACGAG 666
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DB 661 GACGAGAGA 669
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CB255740 650 bp mRNA linear EST 06-NOV-2003
LOCUS CB255740
DEFINITION 23-B012741-027-007-M05-TTR MP12-AD15-027 Arabidopsis thaliana cDNA
clone MP12p772M05TQ 5-PRIME, mRNA sequence.
VERSION CB255740
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Arabidopsis thaliana
AUTHORS Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 650)
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altman, T.,
Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
JOURNAL MEDLINE 22683290
PUBMED 12799357

COMMENT

Contact: Weisshaar B
 ADIS DNA core facility at MPiZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpi-z-koeln.mpg.de
 Insert Length: 650 Std Error: 0.00
 Plate: 7 row: M column: 05
 Seq primer: T7R: CTAATGCACTCACTATAGGA.
 Location/Qualifiers

FEATURES

Source

1..650
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /cuiivar="Eifel-2 (Ei-2)"
 /db_xref="GABI:592595"
 /db_xref="taxon:3702"
 /clone="MPiZp772M0570"
 /tissue_type="whole plant"
 /dev_stage="adult plant, mixed stresses"
 /lab_host="E. coli TOP10"
 /clone_lib="MPiZ-ADIS-027"
 /note="Vector: pSPORT1; Site1: Sali; Site2: NotI; CDNA library from Arabidopsis thaliana, accession Eifel-2; ten week old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a forceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 M-0C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sali-NotI, primer sites and orientation:
 T7-Sali-CCACGCGTCG-5prime-CDNA-polyA-CC-NotI-SP6. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 47.9%; Score 608.4; DB 14; Length 650;
 Best Local Similarity 98.1%; Pred. No. 3.5e-143;
 Matches 626; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 46 ATTATCTCTGCGATCCAGTCTTGTGAGTGAATTCGACGACGAGTCAC 105
 DB 13 ATTATCTCTGCGATCCAGTCTTGTGAGTGAATTCGACGACGAGTCAC 72
 QY 106 TACTCTTGAAGCTTCTCACTACTCCACCGAGTTGTTGGAAATATGATGTAATCTCTG 165
 DB 73 TACTCTTGAAGCTTCTCACTACTCCACCGAGTTGTTGGAAATATGATGTAATCTCTG 122
 QY 166 GAGATGAAGTCAAGACATGACCAAGAGAGCAAAATGTTACTGAAGAGGCGCTT 225
 DB 133 GAGATGAAGTCAAGACATGACCAAGAGAGCAAAATGTTACTGAAGAGGCGCTT 192
 QY 226 GTGCATATGTC-GCCATCTCAAGAGGATATGTTCTCTTAAAGTTGATGTAAGTCGAG 284
 DB 193 GTGCATATGTCGATCTCAAGAGGATATGTTCTCTTAAAGTTGATGTAAGTCGAG 252
 QY 285 GTCTTGATGAGAAAGTCAGTACAGATTAATAAGAGAGTCACGGTTCCAAACATCC 344
 DB 253 GTCTTGATGAGAAAGTCAGTACAGATTAATAAGAGAGTCACGGTTCCAAACATCC 312
 QY 345 AAGTACTCTACATGCTTTTGTCACTACAGGCGACATGACCAAAATCTGCAGCAAAATTT 404
 DB 313 AAGTACTCTACATGCTTTTGTCACTACAGGCGACATGACCAAAATCTGCAGCAAAATTT 372

QY 405 GAGATACATGCGATGAGACGACCAACTTATGTAATGTTCTTGAAAAAGAAAAAGAA 464
 DB 373 GAGATACATGCGATGAGACGACCAACTTATGTAATGTTCTTGAAAAAGAAAAAGAA 432
 QY 465 CTAGCCGTTTACCCATCGGTGTTGCTTACGATGAAGTCTGTGAACGTCGCTTGTGCA 524
 DB 433 CTAGCCGTTTACCCATCGGTGTTGCTTACGATGAAGTCTGTGAACGTCGCTTGTGCA 492
 QY 525 GTTGGCTGGGAATTAACCTTAATGGAAGAAAGAAACCTTTCTTTCCAAATGTTCCACCT 584
 DB 493 GTTGGCTGGGAATTAACCTTAATGGAAGAAAGAAACCTTTCTTTCCAAATGTTCCACCT 552
 QY 585 ATGCGACACTTGTATATGAGGTGAGTAATGTTGCTTGAATGAAACAAAGAGGAAAA 644
 DB 553 ATGCGACACTTGTATATGAGGTGAGTAATGTTGCTTGAATGAAACAAAGAGGAAAA 612
 QY 645 GCTTCGAGTATATGACTGTAGAGGAAGAGATTGTCG 682
 DB 613 GCTTCGAGTATATGACTGTAGAGGAAGAGATTGTCG 650

RESULT 5

CB981020

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Expressed sequence tags from cabernet sauvignon berries at various developmental stages
 Unpublished (2003)
 Contact: Douglas Cook, PhD
 CAES Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: dcook@ucdavis.edu
 Seq primer: GCCAACGATGGCTTAG.
 Location/Qualifiers

FEATURES

Source

1..892
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cuiivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="CAB70003_IVAR_F02"
 /sex="Hermaphrodite"
 /dev_stage="Post-Veraison, 18-19 brix"
 /lab_host="DH5alpha"
 /clone_lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"
 /note="Organ: Berry; Vector: pDNR; Site 1: SfiI; Site 2: 8 SfiI; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGAGTGTATCAACGACAGTGGCATTAACGGCGG-3' and 5'-ATTCTAGAGCGGAGCGGCGGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 38.6%; Score 490; DB 14; Length 892;
 Best Local Similarity 77.0%; Pred. No. 3.7e-113;
 Matches 609; Conservative 0; Mismatches 181; Indels 1; Gaps 1;

163 CTGAGCATCAAACTCAAAACATGACCAAGAGAGCAAAATGTTACTGAAGAGAGTCC 222
 101 CTGCAAGATGCAAAACCTGATCAGAGCATGAAATGATTTACTGAAATGACAGCA 160
 223 GTTGTGATGATGAGCCATC-TCAAGAGGTAATCTCTCTTAAGTGAATGAGAGCT 281
 161 TTGTGTGATGAGGAACTCTTCAAGATGATCGGCTCTCCAAAAGTTGATTCGAAGTG 220
 282 GAGCTCTTGAATGAGAAAGTCAGTACAGATTTAAAGAGAGTCAAGTCCAAACCA 341
 221 GAAGTTTTCATGAGAAAGTCACAAACAGATCTAGAGAGAGTCAATGTCAGAAACCA 280
 342 TCCAAAGTCTCTACATGCTTTTGTCTACTACAGGAGCATGACCAAAAATGCGCAGCA 401
 281 TCCAAATACTCAACATGTTCTTCTGATTAAGGAGCATGAGTGAAGCACCAGCAAG 340
 402 TTGAGAGATCATGAGCATGAGCAGCAACCTATTGATTTGTTCTTGAAGAGAGAGAG 461
 341 TTGAGAGACATGAGAAATGAAACAGTCCAGTTGAAATAGCATAGAGAGAGAGAGAG 400
 462 GAACTAGCCGAGTTAGCATCGGTTGCTAGCATGAAAGTCTGTAAGCGGCTGTG 521
 401 GAAATGACGAGATTTGCTATTGATGCTCTCCAAACATGAGTGTGAGAGAGTCCCTTTTA 460
 522 CATGTTGGCTGGAATTTAGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 581
 461 CATGTTGGCTGGAATTTAGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 520
 582 CCAATGCAACATGTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
 521 CCAATGCAACATGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 580
 642 AAAGCTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 701
 581 AAAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640
 702 GATGAGAGATTTCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
 641 GATGAGAGATTTCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
 762 GCCATGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 821
 701 GCCATGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 760
 822 GCTTTAGCATTTAAAG 881
 761 GCTTTAGCATTTAAAG 820
 882 CGATACGATGAG 941
 821 CGCTAG 880
 942 AAAGCACTGTT 952
 881 AAAGCACTTATT 891

RESULT 6
 AY105475
 LOCUS
 DEFINITION
 Zea mays PCO126622 mRNA sequence.
 AY105475
 VERSION
 AY105475.1 GI:21208553
 KEYWORDS
 HTC.
 SOURCE
 Zea mays
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE 1 (bases 1 to 1363)
 AUTHORS
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitelitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 TITLE
 Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes
 JOURNAL
 Unpublished (2002)
 REFERENCE 2 (bases 1 to 1363)
 AUTHORS
 Coe, E.H.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 COMMENT
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZMDB and may be found by BLAST
 searching at MSL, maizemap.org; ZMDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZMDB:
www.zmdb.iastate.edu.

FEATURES
 source
 1..1363
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeDB:637377"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/Dupont Consensus
 Library"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

ORIGIN
 Query Match 36.6%; Score 464.4; DB 11; Length 1363;
 Best Local Similarity 71.6%; Pred. No. 1.2e-106;
 Matches 637; Conservative 0; Mismatches 251; Indels 2; Gaps 2;

237 CCATCTCAAGAGGTAATGTTCTCTTAAGTGAATGAGAGAGAGAGAGAGAGAGAGAG 296
 222 CTTCCCGAGATGAGCGCCGCCCGGCTTCTCTGACATGAGAGAGAGAGAGAGAGAGAG 281
 297 AAGTCATGAGAGAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 356
 282 AAGTCATGAGAGAGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 341
 357 TGCTTTGTCATACAGGAGATGAGCAAAAATCTCGACACAAATTTGAGATACATGAG 416
 342 TGCTTTGTCATACAGGAGATGAGCAAAAATCTCGACACAAATTTGAGATACATGAG 401
 417 CATGACAGCAACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
 402 CAAGAGCAACATCAATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 461
 477 GCCATGCGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536
 462 GGCATGCGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 521
 537 TTAGCTTATGAG 596
 522 CTAGGCTATGAG 581
 597 TTATATGAG 656
 582 GTTATGAG 641
 657 ATGACCTGTAG 716
 642 ATGACAGTTGAG 701
 717 TTAAAG 776

Db 702 TTCAAAGAAAAAGAGCTTGAGAGAGCCATGACGAAATATGAAATGGCATTTGCATACATG 761
QY 777 GGGAGCAATTTTATGTTTACGCTGTATGAGAGATACAGATATGCTTTAGAGAGTTAA 836
Db 762 GGAATATATTTCAATGTTCAATTTATTTGAAAGATACAGAGACATGGCTGGGCTGAA 821
QY 837 AACCATGCAATCTTAATACATAGCAGCTTGCCTCATCAATAAACGATACGATGAGCA 896
Db 822 AATCATGCAATCTTAATGCTGATGCTGATGCTGATCAATTAAGATTCGATGAGCT 881
QY 897 ATTGTCATCTGCAACATTTGTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 956
Db 882 ATTGCGAGATGATGATTTGTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 941
QY 957 AGAGGAAAGCAAG 1016
Db 942 CGAG 1000
QY 1017 GCACAAAGATGATGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
Db 1001 GCGAAG 1060
QY 1077 CAAG 1126
Db 1061 CAAG 1109

RESULT 7
CF436078
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF436078 972 bp mRNA linear EST 04-SEP-2003
EST672423 normalized cDNA library of onion Allium cepa cDNA clone
ACACD15, mRNA sequence.
CF436078
CF436078.1 GI:34458768
EST.
Allium cepa (onion)
Allium cepa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
Allium.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 972)
Havey, M.J., Cheung, F., Van Aken, S., Uteback, T. and Town, C.D.
Expressed Sequence Tags from a normalized library of mixed onion
tissues (Allium cepa)
Unpublished (2003)
Contact: Havey MJ
Department of Horticulture
USDA-ARS and University of Wisconsin
1575 Linden Drive, Madison, WI 53706, USA
Tel: 608-262-1830
Fax: 608-262-4743
Email: mjhavey@facstaff.wisc.edu
TIGR sequence name ACACD15TR. For more information:
http://havey1ab.hort.wisc.edu
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES
source

Location/Qualifiers
1..972
/organism="Allium cepa"
/mol_type="mRNA"
/cultivar="Red Creole (bulbs), unknown (callus), Ebano &
Texas Legend (roots)"
/db_xref="taxon:4679"
/clone="ACACD15"
/tissue_type="Callus, roots, and young bulbs"
/clone_id="normalized cDNA library of onion"
/note="Vector: pCMVSPORT6.1-ccdb (Invitrogen); Site 1:
ECORV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA
from callus, roots, and young bulbs were combined to
synthesize the library. Normalization to enrich for
low-copy transcripts was performed by proprietary
techniques of Invitrogen."

ORIGIN

Query Match 35.4%; Score 449.6; DB 14; Length 972;
Best Local Similarity 70.0%; Pred. No. 6,5e-103;
Matches 619; Conservative 0; Mismatches 264; Indels 1; Gaps 1;
QY 181 ACAATGACCAAG 239
Db 80 ACTGAGCGCAAG 139
QY 240 TCTCAG 299
Db 140 CTTCAAG 199
QY 300 GTTCAGTACAG 359
Db 200 GTTCATTAACCAATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259
QY 360 TTTTGTCTACAG 419
Db 260 TTTCTTACATTAACAG 319
QY 420 GAGCAGCAACCTAATGATTTGCTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
Db 320 GAAACAAGACCTTTTGAACCTGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 379
QY 480 ATGCGTGTGCTAGCATGAG 539
Db 380 ATTGAGAGTTCAG 439
QY 540 GCTTATGAG 599
Db 440 GATATAGGAG 499
QY 600 TATGAGTGGAG 659
Db 500 TATGAGAGTGGAG 559
QY 660 ACTGTAG 719
Db 560 ACAGTAG 619
QY 720 AAG 779
Db 620 AAG 679
QY 780 GAGAGATTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTAT 839
Db 680 GATGATTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATG 739
QY 840 CCATGCGATCTTAATCAATGAG 899
Db 740 CCATGCGATCTTAATCAATGAG 799
QY 900 GGTCTACTGCAACATTTGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATG 959
Db 800 GGTCTACTGCAACATTTGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATG 859
QY 960 GGAAG 1019
Db 860 GGAAG 919
QY 1020 CAAGAGATGCTCTGAG 1063
Db 920 CAAGAGATGCTCTGAG 963

RESULT 8
CF417393
LOCUS
DEFINITION
ACCESSION
VERSION

CF417393 710 bp mRNA linear EST 02-SEP-2003
USDA-FP-115000-323 Citrus sinensis: Insect-damaged immature
leaves/stems from field collected Valencia orange Citrus sinensis
cDNA clone IDFL-004_5', mRNA sequence.
CF417393
CF417393.1 GI:34418520

KEYWORDS	SOURCE
EST.	Citrus sinensis
ORGANISM	Citrus sinensis
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Citrus. 1 (bases 1 to 710)
AUTHORS	Shatters, R.G. Jr., Chaparro,J.X., Bausher,M.G., Hunter,W.G. and Nledz,R.P.
TITLE	Expressed Sequence Tags from Insect-Damaged Field-Collected Sweet Orange (Citrus Sinensis (L.) Osbeck) Immature Leaves and Stems Unpublished (2003)
JOURNAL	Contact: Shatters, Jr. RG Subtropical Insects Research Unit USA, ARS, U.S. Horticultural Research Laboratory 2001, South Rock Road, Fort Pierce, FL 34945, USA Tel: 772 462 5912 Fax: 772 462 5986 Email: rshatters@usuhrl.ars.usda.gov Seq primer: T3 Primer.
FEATURES	Location/Qualifiers 1..710
SOURCE	/organism="Citrus sinensis" /mol_type="rRNA" /culivar="Valencia" /isolate="mixed field population" /db_xref="taxon:2711" /clone="IDFL-004_G02" /issue type="Flush leaves and stems" /clone.lib="Citrus sinensis; Insect-damaged immature leaves/stems from field collected Valencia orange" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Citrus sinensis (L.) Osbeck; Standard library construction protocols from StrataGene cDNA synthesis kit (cat.# 200401-5) and Uni-ZAP XR vector kit (cat.# 237211) were followed using poly(A) RNA."
ORIGIN	
Query Match	33.8%; Score 429; DB 14; Length 710;
Best Local Similarity	76.5%; Pred. No. 1e-97;
Matches	539; Conservative 0; Mismatches 165; Indels 1; Gaps 1;
Dn	423 CAGCAACCTATTGAATTTGGTCTTGGAAGAAGAAAAAAGAACTAGCCGTTTAGCCATC 482 1 CAACAACCGCTGGAATGTTTAGAAAAGAAAAAGAAAGATGACTGCCTGGCTATT 60
Qy	483 GGTTGTGTACATGAAAGTCGTGGAAGTCGCCGCTTGCAATGTTGGCTGGGAANTTACT 542 61 GGGGTGTACACATGAAGAGCTGTGTAACATGACTGTTCATGTGGCTGGGAANTTGGGT 120
Dd	543 TATGGGAAGAAGAAACCTTTTCTTTTCCCATGTTCACCTATATGGCAGACTTGTATAT 602 121 TATGGGAAGAAGAAAGCTTTTCTTTTCCCAATGTGTCTCCATGTGCAACTAGTATAT 180
Db	603 GAGGTGGAAGTTATTGGTTGATGAACAAGAAGGAAAAAGCTCGAGTGATATGACT 662 181 GAGGTGTGTGCATATGGCTTTGACGAACCAAGAAAGGAAAAAGCTCGATGACATGACT 240
Qy	663 GTAGAAGAAAGATTGGTGTGCAAGCAGACGAAGAAGAAAAATGATGGGAATTCCTTTTAA 722 241 GTCAAGAAAGAAAGATTGGTGTGCAAGCAGACCGAAGAAAGATGATGAAATGCTTATTAA 300
Dd	723 GAGGAAGAACTGGAAGAGCCATGCAACAGTATGAATGGGCATATGATGATGAGGAGAC 782 301 GAGGAAGAACTGGAAGAGCCATGCAACAGTATGAATGGGCATATGATGAGGAGAC 360
Qy	783 GATTTATGTTTCAAGCTGTATGGGAAGTACAGATATAGCTTTAGCATTAATAAACCA 842 361 GACTTCATGTTTCAAGTTGTTTGGGAAGTACCGGAGTATAGCTTTGGCTGTTAAGATCA 420
Dd	843 TGCCATCTTAACATGACGCTTGTCTCATCAAATCTAAGACATACATGATGATGATGAT 902 421 TGCCATCTTAACATGACGCAATGCTTATTAAGCTCAAAAGCTTTAAGAAAGACCATGGG 480

Oy		903	CACGCAACAATTGGCTTGACAGAAAGAAGAAAAACCCAAAGCAGCTTTCAGAAAGAGGG	962
Db		481	CAATGCAGCCCTGTATTGGAGAGAGATGAATAATATGTGAAGGCCCTTTTCAGACAGAGA	540
Oy		963	AAMGCAAGGCAGAGCTAGGACAGATGTAAGTCTCAGCACGTGATGATTTCCGAAAAGSCAACAA	10222
Db		541	AAGCTTAGACAGAGAACTTGGGCAAAAGCATGCTGCCGGGAAGACTTTCTTAAGAGCAGGT	600
Oy		1023	AAGTATGCTCTGACGACGAAAGCGATTAGA-AGAGAGCTACGAGCACTTGCAGAGCAGAA	10811
Db		601	AAATTTCACCTTGTAAGCAATCAATTGAGACGGGGACCTTCGTTTGCTCGTGAACATGA	660
Oy		1082	GAAAGCCTTGATACCAAAAGCAGAAAGAAATGTACAAAGAGATATT	1126
Db		661	AAAAGCTGTATACAGAGCAAAAAGAGATCTAATAGAAATTTTT	705
RESULT 9				
CA765208				
LOCUS				
DEFINITION	CA765208	839 bp	mRNA	linear EST 08-JAN-2003
KEYWORDS	AF53-Rpf_06_K05_T7_029.abl IRRI Drought Stress Panicle Library			
ACCESSION	Oryza sativa (indica cultivar-group) cDNA clone C0002165 5' similar to 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (peptidylylprolyl cis-trans isomerase) (Cyclophilin) (PPIase), mRNA sequence.			
VERSION	CA765208			
SOURCE	CA765208.2 GI:27546946			
ORGANISM	EST.			
REFERENCE	Oryza sativa (indica cultivar-group)			
AUTHORS	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza.			
TITLE	1 (bases 1 to 839)			
JOURNAL	Bennett,J., Arumugam,K., Laflitte,R., Wen,J., Rudd,S. and Bruskiewich,R.M.			
COMMENT	IRRI Drought Stress Panicle cDNA Library Unpublished (2002) On Dec 2, 2002 this sequence version replaced gi:25994463. Contact: Richard Bruskiewich Biometrics and Bioinformatics Unit International Rice Research Institute DAPO 7777, Metro Manila, Philippines Tel: +63-2-845-0563 Fax: +63-2-845-0606 Email: r.bruskiewich@cgiar.org International Rice Information System (IRIS; http://www.iris.irri.org): DO202164 Assignment of putative function to the sequence by S. Rudd of the Munich Information Center for Protein Sequences (http://mips.gsf.de) Plate: 06 Row: K Column: 05.			
FEATURES				
Source	Location/Qualifiers			
	1..839			
	/organism="Oryza sativa (indica cultivar-group)"			
	/mol_type="mRNA"			
	/cultiyar="IR64"			
	/db_xref="taxon:39946"			
	/clone="C0002165"			
	/issue_type="Panicles"			
	/dev_stage="Flowering"			
	/clone_lib="IRRI Drought Stress Panicle Libray"			
	/notes="Vector: pBluescript II SK+; Water stress was applied by not watering for 4 consecutive days. Panicles were collected from control (well watered) and stressed plants at 2 days before heading, at heading, 50% flowering and 4 days after 50% flowering."			
ORIGIN				
Query Match	31.1%; Score 395.6; DB 14; Length 839;			
Best Local Similarity	74.4%; Pred. No. 3,1e-89;			
Matches 511; Conservative	0; Mismatches 175; Indels 1; Gaps 1;			

QY 441 GTTCTGGAAAAAGAAAAAGAACTAGCCGGTTTACCATCGGTGTTGTAGCATGAG 500
Db 21 GTAATGGAAAAAGAAAAAGAACTAGCTGTGTTAGGCAATGGTGTGTAACATGAGA 80
QY 501 TCTGTGAACGTGGCTTGTGTCATGTTGGCTGGGAATTAAGTTATGGAAAAAGAAAC 560
Db 81 AGTGGGGAGCACTGTTGCGTGGTGGCTGGAGCTAGGCTATGGAAAAAGAAAGGAGC 140
QY 561 TTTTCTTTTCCCAATGTTCCACTATAGGCACTTTGTTATATGAGAGTGAAGTTATTGG 620
Db 141 TTTTCATTTCCCAATGTTCCCTCCCAATGSCAATCTTTATATGAAAGTTGAATTTGGG 200
QY 621 TTTGATGAACAAAGAGGAAAAAGCTCGCATGATATGACTGTATGAGAAAAAGATTGGT 680
Db 201 TTTGATGATGTCAAAGAGGAAAAAGCCGGAAGTACATGACATGAGAGAAAGGATTGAA 260
QY 681 GCACAGACAGAAAAAGAAATGAGTGGAAATCTCTTTTAAGAGAGAAACCTGAGAA 740
Db 261 GCAGCGGACAGAGAGAGATTTGAGGGCAATGATATTTCAAAGAAAAAGATTGAGAG 320
QY 741 GCCATGCAACAGTATGAATGGCCATAGCATATACATGAGGAGCAATTTATGTTCACTG 800
Db 321 GCCATGCAACAGTATGAATGGCCATAGCATATGAGGAGCAATTTATGTTCACTG 380
QY 801 TATGGGAATGACAGAGATATGCTTTAGCACTTAAAAAAGCCATCCATTTTACATGACA 860
Db 381 TTTGGGAAATACAGAGATATGCTTGGCTGTGAAAAATCCATGTCATCTCAACATGGCC 440
QY 861 GCTTGGCTTCATCAATCTAAACGATATGATGAAACCAATTTGCTCACTGCAACA-TTGTGTT 919
Db 441 GCATGCTCAATCAACCTGAAGAGATTCGATGAACTTCGACAGTATGATTTGTTGTT 500
QY 920 GACAGAAAGAGAAAAAAGCCAAAAAGCACTGTTCAAGAAAGAGAAAAAGCAGAGCT 979
Db 501 GCGAGAGGATTAATTAATGTAAGCACTTTTTCAGAGAGAAAAAGCAGAGCTGAACT 560
QY 980 AGGACAGATGAGCTCAGACCTGATGATTTTCGAAAGGACAAAAAGTATGCTCTGACA 1039
Db 561 TGCTCAGACAGAAATCAGGAGGAGGAGCACTTCTGAAAGCCAAAGAAATCTCCAGAGA 620
QY 1040 CAAGGCGATTTAGAGAGGCTAGAGCACTTGACAGAGCAAGAAAGCTTTGTAACAAA 1099
Db 621 CAAGGAGATCCAGGAGTGTGCTTGGCTCTGCGGAAACAGATTAAGCTGTACCAAAA 680
QY 1100 GCAGAGAAATGTACAAAGGAATATT 1126
Db 681 ACAGAGAGAGCTGTACNAAGGCTCTT 707

RESULT 10
AM773636 650 bp mRNA linear EST 07-SEP-2000
LOCUS EST332622 KV3 Medicago truncatula cDNA clone pKV3-15123, mRNA
DEFINITION
ACCESSION AM773636
VERSION AM773636
KEYWORDS
SOURCE
ORGANISM
EST.
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 650)
Vandenbosch, K., Hutt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
ESTs from roots of Medicago truncatula after Rhizobium inoculation
Unpublished (1999)
Contact: Vandenbosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA

FEATURES
source
1..650
/organism="Medicago truncatula"
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meliloti"
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/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI: cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the UniZap XR vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."

ORIGIN
Query Match 30.8%; Score 391.6; DB 10; Length 650;
Best Local Similarity 75.3%; Pred. No. 3.1e-88;
Matches 487; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 403 TTGAGATATCATGSCATGAGAGAGCAACCTATGATTTGTTCTTGGAAAAAGAAAAAG 462
Db 2 TTGAGATATCATGSCATGAGAGAGCAACCACTGATGTAATGTAAGAAAAAGAAAAAG 61
QY 463 AACTAGCCGTTTATGACCATGCTGTTGCTTATGATGAAAGTCTGTAAGCTGCTTGTGC 522
Db 62 AATGACTGCTTGGGCACTTGGGCTGGCAAGATGAAGCGGGGAGCGAGCATTTGTCG 121
QY 523 ATGTTGGCTGGGAATTAAGCTTATGAGAAAGAAAGAAACCTTTCTTTCCCATGTTCCAC 582
Db 122 GTGTAACTGGGGAATTAAGATATGACAGAGAAAGAAAGCTTTTCAATTTCCAAATGTTCCAC 181
QY 583 CTATGAGAGACTGTTATATATGAGTGAAGTATTTGGTGTATGAAACAAAGAGAGGAA 642
Db 182 CAATGGCAATTTAGTTATATGAGTTGAGCTCATTTGTTTATGTAACAAAGATGGA 241
QY 643 AAGCTCGAGTGAATATGACTGTAGAGAAAGATTTGTCAGAGACAGAGAAAAATAG 702
Db 242 AAGCTCGAGTGAATATGACTGTAGAGAAAGATTTGGGCAAGGATCGAGAAAGATAG 301
QY 703 ATGGAATTTCTCTTTTAAAGAGAGAAAGCTGAGAGAACCATGCAACGATTAATAG 762
Db 302 ATGGAATTTCTCTTTTAAAGAGAGAAAGCTGAGAGAACCATGCAACGATTAATAG 361
QY 763 CCATACATATACATGAGGAGAGATTTATGTTTCACTGATAGGAAAGTACAGGATATAG 822
Db 362 CCATACATATATGAGGAGAGATGACTTATGTTTCACTGATAGGAAAGTATAGGATATAG 421
QY 823 CTTTACAGTAAAAAAGCCATGCACTTATACATAGCACTTGCCATCAAACTAAAC 882
Db 422 CTCTGCTGTAAAGATTCATGCACTTAAACAGCGCGGCTGTGATTAAGCTGAAC 481
QY 883 GATACATGAAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAACCAA 942
Db 482 GCTATGAAGAGATATAGCAATGATGATGATTAAGTGAAGAGAGCAACAAATTTGA 541
QY 943 AAGCACTTTTCAAGAAAGGAAAGCAAGAGAGAGCTAGAGAGATGAGCTAGAGAGCG 1002
Db 542 AGGCTTTATTTAGAGAGGATTAAGGCTTAGAGAGAGCACTGGGAGAGAGATGCTAGCG 601


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Db 108 AAGATGATGAAAATGAAAAGCTATGAGAAAGCTGCGCTTGCTGCTGAGCTTTGCG 167
Qy 244 AAGAGGTTATGTTCCCTTAAGTATGTAAGCTGAGGCTTGGATGAGAAATGCA 303
Db 168 AAGTGGGAATCATCTCCGAAAGTCCAAATCCGGGTGTAATCTTCAAGAGAAATGCA 227
Qy 304 GTAAGCAGATTATTAAGGAAGTCAAGCTTCCAAACATCCAAAGTACTTACATGCTTTT 363
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Db 348 AACCAACATTTGAAATGCTTTTAAAGAAAAAGAAAGAAATGAATGCGGGTTTACCTTTG 407
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Db 648 AGGAAAACTTGAAGAGGCTATGACAGCATGTAATGCAATTTGATTTGGGCGA 705

RESULT 13
LOCUS B0994520
DEFINITION B0994520 699 bp mRNA linear EST 21-AUG-2002
ACCESSION OQ67H10.YS.ab1 OQ_EFGHU lettuce serritola lactuca sativa cDNA clone
VERSION B0994520
KEYWORDS B0994520.1 GI:22414055
SOURCE EST.
ORGANISM Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 699)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., Van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lei,Z., Church,S., Jackson,L. and Bradford,X.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Aamundson Hall, UCD, Davis, CA 95616, USA
tel: 1-(530)-742-1742
fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OQ_CA_contig5377, see http://cgpdb.ucdavis.edu/
for details.
Plate: OQ67 row: H column: 10.
Location/Qualifiers
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/clone_1nb="OQ_EFGHU lettuce serritola"
/note="Vector: pBRCDNA5flab; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_L1nb=OQ_EFGHU lettuce serritola
TAG_SRO=GCTTGACGGG"

ORIGIN
Query Match 27.9%; Score 354.4; DB 13; Length 699;
Best Local Similarity 71.4%; Pred. No. 8.3e-79;
Matches 466; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

474 TTAGCCATCGGTGTTCTAGCATGAACTGTGTAACGTCGCTTGTGATGTTGCTG 533
2 TTGGCCATTCGCTTGAGCTCCATGAAATCGGGGAGCGAGCTGTATCATGTGGTTG 61
534 GAATTAGCTTATGGAAGAAAGAACTTTCTTTTCCCAATGTTCCACTATGCGAGC 593
62 GAATTAGGATGATGTAAGAGAAAGAACTTTCTTTTCCCAATGTTCCACTATGCGAAT 121
594 TTGTTATAGAGGTGGAAGTTATGTTGCTTGAAGAAACAAAGAGGAAAAAGCTGCGAGT 653
122 ATATCTATGAAATGCAACTAATGCTTTTGAATGAAACAAAGAGAAAGAAAGCTCGAGT 181
654 GATATGACTGTAGAGAAAGATTTGCTGACGACAGACAGAAAGAAATGATGGAATTTCT 713
182 GATATGACTGTAGAGAAAGATTTGCTGACGACGACGATGAAAGAAATGATGGAATTTCT 241
714 CTTTATAGAGGAGAAAGAACTGAGAGAAAGCCATGCAACATGTAATGCGCATATGCAATC 773
242 TTGTTCAAGAGAAAGAAATTTAGAGAGGCTATGCAACATATGAAATGCAATCGCATATC 301
774 ATGGGGAAGATTTTATGTTTTCGCTGATGGAAGTATGCAAGATATGCTTTAGAGATT 833
302 ATGAATGATGATTTCAATGTTTCAATTAATGAAAGTATCAAGCATGCTTTAGCAGTT 361
834 AAAAACCATGCTCATTTAATACATAGCAGCTTGCCTCATCAAACTAAAGATAGATGAA 893
362 AAGAACCTTTGTACCTTAAACATGTCAGCTTTGTTGATAAGCTCAAGCGTATGAAAG 421
894 GCAATTTGTCATGCAACATTTGTTGACAGAAAGAAAGAAAGAAAGCAAGCACTGTTTC 953
422 GCCATTGCTCAAGTCTATTTGATCTTTGAGAGATCAAAATATGTAAGAGCATATTTT 481
954 AGAAGGGAAGAAAGCAAGGAGGCTAGACAGATGAGTCAAGCTGACGATGATGTTCCGA 1013
482 AGCGAGGGAAGAACTCGGTGAGACTCGGCAACGAGATGCTGCCGAGAAAGATTTTTCG 541
1014 AAGGCAAAAAGTATCTCTGACGACAAAGGCGATTTAGAGAGAGCTAGAGCATTTGCA 1073
542 AAGCGCGTAAATTTTCCCTGTAAGATTAAGCAATTTGAGGAATTTGGTGTGCTTTAT 601
1074 GAGCAAGAGAAAGCTTTGTAACAAAGCAAGAAAGAAATGTACAAAGGAATATT 1126
602 GAAGATGATTAAGTTGTTTATGAGAAACAAAGAGAGCTTTATTAAGGCTTGT 654

RESULT 14
BG451848
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LOCUS BG451848 667 bp mRNA linear EST 16-MAR-2001
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 5', mRNA sequence.
 ACCESSION BG451848
 VERSION BG451848.1 GI:13370630
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 1 (bases 1 to 667)
 REFERENCE Torres-Jerez, I., Scott, A. D., Harris, A. R., Gonzales, R. A., Bell, C. J., Flores, H. R., Imman, J. T., Weller, J. W. and May, G. D.,
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula drought library
 Unpublished (2000)
 JOURNAL Contact: May GD
 COMMENT Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
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 249 AGGCGATGCTGTGAGAACGAGACCAAAATTTGAAATACATGCGCAGGACCAACGACCA 308
 QY 432 ATTGAATTGCTTCTTGAGAAAGAGAAAAAGAACTAGCCCGTTTACCGCATCGGTGTGCT 491
 309 ACTGAGATGCTAATAGAGAAAGAGAAAGAAATAGCTGCTTGCGCATTTGGGGTGGCA 368
 Db 492 AGCATGAAGTCTGTGAGAACTGCGCTTGTGATGCTTGGCTGGAGATTAGCTTATGGGAAA 551
 369 AGCATGAAGCGGGGAGCGAGCATTTGTCGTGTAGCTGGGAAATTAGGATATGACAG 428
 QY 552 GAGGAAAGCTTTCTTTCCATATTTCCACCTATGSCAACAATGTTATATGAGGGTGA 611
 429 GAGGAAAGCTTTCTTTCCATATTTCCACCTATGSCAACAATGTTATATGAGGGTGA 488
 Db 612 GTTATTTGGTTTATGAGAAAGAGAGAGAAAGCTCGCATGATATGACTGTAGAGAA 671
 489 CTGATTTGGTTTATGAGAAAGAGAGAGAAAGCTCGCATGATATGACTGTAGAGAA 548

QY 672 AGGATTTGTCAGCAGACGAGAAAGAAATGATGGAAATTTCTTTTAAAGAGAGAA 731
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 Db 549 CGGATTTGGGCGACCGATCGAGAAAGATGATGAAATCTTTGTTTCAAGA-AATTA 607
 QY 732 CTGAGAAAGCCATGCAACAGTATGAATGCGCATGATGAGGAGAGATTTTATG 791
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 RESULT 15
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 DEFINITION Pfaijxoj189E0909 Poplar cDNA library from young opposite xylem
 Populus alba x Populus tremula cDNA 5', mRNA sequence.
 ACCESSION CF234356
 VERSION CF234356.1 GI:33453785
 KEYWORDS EST.
 SOURCE Populus alba x Populus tremula
 ORGANISM Populus alba x Populus tremula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 1 (bases 1 to 493)
 REFERENCE Dejardin, A., Leprie, J.-C., Lesage-Descauses, M.-C., Costa, G. and Pilate, G.
 Expressed sequence tags from poplar tension wood tissues - A comparative analysis from multiple libraries
 Unpublished (2003)
 JOURNAL Contact: Leprie JC
 COMMENT Unit of Forest Improvement, Genetics and Physiology
 National Institute for Agricultural Research (INRA)
 Domaine de Limere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
 Tel: 33 02 38 41 78 00
 Fax: 33 02 38 41 78 79
 Email: Jean-Charles.Leprie@orleans.inra.fr
 PCR Primers
 FORWARD: TriplexA 5' CTCGGAAGCGCGCCATTTG 3'
 BACKWARD: TriplexB 5' ATACGACTCATTATGAGGCGA 3'
 Plate: Pfaijxoj1 row: B column: 9
 Seq primer: TriplexA 5' CTCGGAAGCGCGCCATTTG 3'.
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 /sex="female"
 /tissue_type="Young differentiating xylem harvested on opposite wood side of tilted trees"
 /dev_stage="3-years-old poplar trees grown in the nursery"
 /clone_lib="Poplar cDNA library from young opposite xylem"
 /note="A cDNA library was made with mRNA isolated from opposite wood tissues corresponding to the differentiating xylem collected with a scalpel after debarking the stem. The sampling was done on 3 different tilted trees grown in the nursery. cDNAs were cloned in an oriented way into SfiI (A and B) restriction sites. A one-step conversion of Lambda Triplex2 to the corresponding Triplex2 plasmid was done via site-specific recombination at loxp sites (Clontech; SMART cDNA library construction kit). cDNA inserts were PCR amplified using flanking primers and then sequenced on a ABI3100 Genetic Analyser (Applied Biosystem)"
 ORIGIN
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 Best Local Similarity 79.3%; Pred. NO. 1.7e-73; Indels 0; Gaps 0;
 Matches 391; Conservative 0; Mismatches 102;
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 Db 1 GCTGTTGGTGTTCGATGAGAGCTGGTGAACGTCCTTTCATCATGTCGCTGGAA 60

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QY 537 TTAGCTTATGGAGAAAGAGAACTTTTCTTTTCCCATGTTCCACCTATGCGAGACTTG 596
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QY 597 TTATATGAGGTGAGAGTTATTTGGGTTTGATGAACAAGAGGAAAAGCTGCGAGTAT 656
Db 121 AATATGAAAGTCAGCTTATTTGATTTGAAGTCAAAGAGGAAAAGCTCGTGAT 180
QY 657 ATGACTGTAGAGAAAGATTTGTCAGCAGACAGAAAGAAAATGATGGGAATTCTCTT 716
Db 181 ATGACTGCAAGAAAGATCGGCGAGATCGAAGAAAATGATGGAATTCCTA 240
QY 717 TTTAAGAGAGAAACTGAGAAAGCCATGCAACAGTATGAATGGCCATAGCATACATG 776
Db 241 TTCAAGAGAGAAAACCTTGAGAGGCTATGCAAGCANTATGAATGGCAATTGCATATTG 300
QY 777 GGGAGCGATTTTATGTTTCAGCTGTATGGAGATACCGAGATATGCTTTAGCAGTTAA 836
Db 301 GGTGACGACTTTATGTTTCAGCTGTGTTGGCAAGTACCGAGACATGGCATTGGCAGTAA 360
QY 837 AACCCATGCCATCTTAACATAGCAGCTTGCTCATCAAACTAATAACGATACGATGAAGCA 896
Db 361 AATCCATGTCATCTTAACATAGCAGCTTGCTCATCAAGCTTGAGCGCTATGANAAGCC 420
QY 897 ATTGTCACCTGCAACATTTGTTGACAGAGAGAGAAAACCCAAAAGCACTGTTGAGA 956
Db 421 ATTGCACATGCAACATTTGTTGTTGANGATGAAGAAACAAATGCTAAGGCTTTGTTGAGA 480
QY 957 AGAGGAGAAAGCAA 969
Db 481 ANAGGAGAAAGCCA 493
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